SEARCH REQUEST FORM

| | Serial Number: | - | Requestor's Name: |
|-------------------------------------|-----------------------------|-----------------------|---|
| rt Unit: | | Phone: | Date: |
| ot matter to be compled. Define any | rifically as possible the s | rch tonic. Describe s | Search Topic: |
| o | ent citations, authors, ke | Give examples or re | Please write a detailed statement terms that may have a special map please attach a copy of the sequence. |

Shears, Beverly



From: Sent: To: Subject:

Devi, Sarvamangala Wednesday, January 28, 2004 9:02 AM Shears, Beverly 09/359,426

Beverly:

Would you please perform a sequence and an interference search on SEQ ID NO: 2 in application SN 09/359,426?

S. DEVI, Ph.D. AU 1645 Remsen - 3B07



STIC Search Repo

STIC Database Tracking Number 1.12984

To:

Sarvamangala Devi

Location: REM 3B07

Art Unit: 1645

Friday, January 30, 2004

Case Serial Number: 09/359426

From: **Beverly Shears**

Location: Remsen Bldg.

RM 1A54

Phone:

571-272-2528

beverly.shears@uspto.gov

| | STAFF USE ONLY | |
|--------------------------|----------------|--------------|
| Date completed: 01-29-04 | Search Site | Vendors |
| Searcher: Bevery @ 2528 | STIC | IG |
| Terminal time: 2.2 | CM-1 | STN |
| Elapsed time: | Pre-S | Dialog |
| CPU time: | Type of Search | |
| Total time: 25 | N.A. Sequence | APS |
| Number of Searches: | • | Geninfo |
| | A.A. Sequence | SDC |
| Number of Databases: | Structure | DARC/Questel |
| • • | Bibliographic | Other CGN |

THIS PAGE BLANK USERO

09/359426

(FILE 'REGISTRY' ENTERED AT 15:43:31 ON 29 JAN 2004)

L2 1 S EEKTPLTTAA.APVV.NA/SQSP

FILE 'HCAPLUS' ENTERED AT 15:44:32 ON 29 JAN 2004

L3 1 S L2

L3 ANSWER 1 OF 1 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1998:527345 HCAPLUS

DOCUMENT NUMBER: 129:160619

TITLE: Pseudomonas aeruginosa antigen

INVENTOR(S): Cripps, Allan William; Kyd, Jannelle; Dunkley, Margaret; Clancy, Robert Llewellyn

PATENT ASSIGNEE(S): Auspharm International Limited, Australia;

Chapman, Paul William SOURCE: PCT Int. Appl., 23 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent LANGUAGE: English

FAMILY ACC. NUM. COUNT: 2

PATENT INFORMATION:

| | PAT | ENT 1 | 10. | | KII | ND | DATE | | | APPLICATION NO. DATE | | | | | | | | | |
|------|--|-------|------|------|--------|-------|----------|-------|-------------|----------------------|-------|-------|------------------|--------------------|---------|--------------|-------|--|--|
| | WO | 9832 | 769 | | A: | 1 | 1998 | 0730 | | W | 0 19 | 98-GI | B217 | | 1998 | 0126 | | | |
| | | ₩: | AL, | AM, | AT, | AU, | AZ, | BA, | BB, | BG, | BR, | BY, | CA, | CH, | CN, | CU, | CZ, | | |
| | | | DE, | DK, | EE, | ES, | ΕΊ, | GB, | GE, | GH, | GM, | GW, | HU, | 10, | IL, | 15, | UP, | | |
| | | | KE, | KG, | KP, | KR, | KZ, | TC, | LK, | LК, | LS, | LT, | TO, | ΓΛ, | MD, | MG, | ML, | | |
| | | | MN, | MW, | MX, | NO, | NZ, | PL, | PT, | RO, | RU, | SD, | SE, | 36, | SI, | DV, | SL, | | |
| | | | | | | | | UG, | US, | UZ, | VN, | YU, | ZW, | ΑM, | ΑZ, | BI, | NG, | | |
| | | | KZ, | MD, | RU, | ΤJ, | TM | | ~- | | ~ | | 5.5 | ~ | D.F. | DI | пс | | |
| | | RW: | GH, | GM, | KE, | LS, | MW, | SD, | SZ, | UG, | ZW, | AT, | BE, | CH, | DE, | DK, | ES, | | |
| | | | | | | | | | | | | | SE, | Br, | ВJ, | CF, | CG, | | |
| | | | | | | | ML, | | | | | | 0 77 | | 1000 | 0100 | | | |
| | ZA | 9800 | 587 | | A | | 1999 | 0/23 | | Z. | A 19 | 98-5 | 8 / i = 1 = 1 | | 1998 | 0126 | | | |
| | AU | 9857 | /17 | | Α. | 1 | 1998 | 0818 | | A | 0 19 | 98-5 | //1/ | 0 | 1000 | 0126 0126 | | | |
| | EΡ | 98038 | 39 | | Α. | 1 | 2000 | 0223 | | E | 5 19 | 98-91 | 013/ | 7 11 | יסכנו | J126 | MC | | |
| | | R: | | | | DE, | DK, | ES, | FR, | GB, | GR, | IT, | LΙ, | ĿŲ, | NL, | SE, | MC, | | |
| | | | PT, | IE, | FI_ | _ | 0001 | | | - | D 10 | 00 5 | วา <i>ก</i> / : | 1 | 1000 | 0126 | | | |
| | | 2001 | | | | | | | | J D 1 | P 19 | 98-5. | 31 /4. | T_ | 1998 | 0124 | | | |
| PRIO | RITY | APP | LN. | INFO | . : | | | | | GB T | 991- | 1489 | , | A. | 1997 | 0126 | | | |
| | | _ | | _ | _ | _ | | | | | | | | | 1998 | | | | |
| AB | An | ovel | ant. | igen | iro | n P. | aer | ugin | osa . | ıs p | rovi | aea. | TH | e us | e or | the | | | |
| | ant | igen | in | dete | cting | g/di | agno | sing | Ρ., | aeru | gino | sa a | s, we. | TT g | SIL | s use | e Tu | | |
| • | | citi | | | | | pons | e are | e al: | so p | rovi | aea. | | | | • | | | |
| IT | 211 | 046-3 | 36-5 | D, d | eriv | 5. | 11777 // | TI | - ·- ·- · · | | | . DT/ | ΩT /1 | D 1 ~ 1 | oaia | _ 1 · | | | |
| | | PRP | | | |); 1 | HU (| rner | apeu | tic | use | ; br |) TC | PIOI | .ogic | 31 | | | |
| | stu | ıdy); | | | | | | | | £ | | | ~~ ~ | ~~ + | root | ina | | | |
| | | (Psei | idom | onas | aerı | ugın | iosa | anti | gen | ior | alag. | HOST | ib ma | nu t | reat. | ing | \ | | |
| | | Pseud | | | | | sa 1 | niec | tion | ın | cyst | IC I | TOTO | 515 | harı | BHUS. |) | | |
| RN | 211 | 046-3 | 36-5 | HC. | APLU: | 5 | VI | | m | la a m | ۸ مما | 1 n n | 1 | ~ ~ ~ [~] | 1 a - D | ro-17 | - l - | | |
| CN | | tide | | | | | | | | | nr-A | та-А. | ⊥a-X∂ | aa-A | та-Р | TO-0 | a 1 - | | |
| | Val-Xaa-Asn-Ala) (9CI) (CA INDEX NAME) | | | | | | | | | | | | | | | | | | |

SEQ 1 EEKTPLTTAA XAPVVXNA

THIS PACK BLANK USETU

09/359426

REFERENCE COUNT:

THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> fil hom FILE 'HOME' ENTERED AT 15:45:23 ON 29 JAN 2004

Shears 571-272-2528

THIS PAGE BLANK USTU

Title: Perfect score:

Run on:

Scoring table: Sequence:

Searched:

Database

Devis.

Sequence 125872

Sequence Sequence

Sequence Sequence

Sequence Sequence

Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence

Sequence Sequence

Sequence

Sequence

Sequence

1D 2 "

Seg. 1D

```
US-10-366-683-21327

US-10-419-1282-1327

US-09-543-611A-4268

US-10-603-114-4268

US-10-282-122A-77773

US-09-791-537-30924

US-10-282-122A-77773

US-10-282-122A-77777

US-10-360-039-13806

US-60-360-039-13806

US-60-360-039-13806

US-10-437-965A-35912

US-10-437-96A-35912

US-10-049-750-123

US-10-049-750-123

US-10-049-750-123

US-10-049-750-123

US-10-138-077-23364

US-10-38-077-23364

US-10-38-077-23364

US-10-38-077-23364

US-10-38-077-23364

US-10-31-96A-35910

US-09-708-427-2365

US-10-31-96A-346

US-10-31-96A-346

US-10-31-96A-346

US-10-31-96A-346

US-10-31-96A-346

US-10-31-96A-346

US-10-156-76L-10589

US-09-708-427-80045

US-09-708-427-80045

US-09-708-427-80045

US-09-708-427-8045

US-09-708-427-8045

US-09-708-427-8045

US-09-708-427-8045

US-09-708-427-8045

US-09-708-427-8045

US-09-708-427-8045

US-09-708-427-27614
US-09-791-537-125872
US-10-366-683-21327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /3-655A-1483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2. Application US/09359426C
GENERAL INFORMATION:
APPLICANT: Cripps, Alan William
APPLICANT: Clancy, Robert Llewellyn
APPLICANT: Clancy, Robert Llewellyn
APPLICANT: Dunkley, Margaret
TITLE OF INVENTION: Antigen
FILE REPERENCE: A33655 064727.0105
CURRENT FILING DATE: 1999-09-14
FRIOR APPLICATION NUMBER: US/09/359,426C
CURRENT FILING DATE: 1999-01-26
PRIOR FILING DATE: 1998-01-26
PRIOR FILING DATE: 1997-01-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID 0.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
      TYPE: PRT ORGANISM: P. Aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-359-426C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: I
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 19
                                                                                                                                                                                                         January 28, 2004, 13:09:30 ; Search time 171 Seconds (without alignments) 101.102 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5728757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6/ptodata/1/paa/US087_COMB.pep:*
6/ptodata/1/paa/US088_COMB.pep:*
6/ptodata/1/paa/US088_COMB.pep:*
6/ptodata/1/paa/US089_COMB.pep:*
6/ptodata/1/paa/US091_COMB.pep:*
6/ptodata/1/paa/US092_COMB.pep:*
6/ptodata/1/paa/US093_COMB.pep:*
6/ptodata/1/paa/US095_COMB.pep:*
6/ptodata/1/paa/US095_COMB.pep:*
6/ptodata/1/paa/US095_COMB.pep:*
6/ptodata/1/paa/US095_COMB.pep:*
6/ptodata/1/paa/US095_COMB.pep:*
6/ptodata/1/paa/US095_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pending_Patents_AA_Main:*

1: /cgn2_6/ptodata/1/paa/USO6_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/USO6_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/USO8_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/USO8_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/USO8_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/USO82_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/USO83_COMB.pep:*
8: /cgn2_6/ptodata/1/paa/USO83_COMB.pep:*
9: /cgn2_6/ptodata/1/paa/USO83_COMB.pep:*
9: /cgn2_6/ptodata/1/paa/USO83_COMB.pep:*
9: /cgn2_6/ptodata/1/paa/USO83_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             paa/US098 COMB.pep:*
'paa/US099A COMB.pep:*
'paa/US099B COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /paa/US100_COMB.pep:
                                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5728757 segs, 909918778 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/1/paa/US104
/cgn2_6/ptodata/1/paa/US106
/cgn2_6/ptodata/1/paa/US60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                1 XEEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (cgn2_6/prodata/1/

(cgn2_6/prodata/1/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ptodata/1/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ptodata/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ptodata/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                           US-09-359-426C-2
81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 :: 116 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 117 :: 11
```

Sequence (

Sequence

Sequence

Sequence Sequence

Sequence Sequence Sequence Seguence

Sequence

sequence

DOMAIN

Sequence 2, Appli

19 17 US-09-359-426C-2

93.8

Score 92

Result Š.

Sequence Sequence

Sequence Sequence

Sequence

```
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABII
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILLE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
                                                                                                                                                                                                                                                                                         RELATING TO PSEUDOMONAS
                    ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                              APPLICANT: Marc 1. Rubenfield et al.

APPLICANT: Marc 1. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/010/419,128

CURRENT FILING DATE: 1099-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

SEQ ID NO 21327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 19; Length 406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.057;
82.4%; Pred. No. 0.057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 53; DB
Pred. No. 2.7;
                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 63;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 4268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4268, Application US/09543681A GENERAL INFORMATION:
                                                                                                                                                                                                                      Sequence 21327, Application US/10419128 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-603-114-4268; Sequence 4268, Application US/10603114; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 EEKTRLTTAAGAPVVDN 18
                                                                                                          2 EEKTRLTTAAGAPVVDN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77.8%;
82.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 EKKKLTTAAGAPVVDN 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 EEKTPLTTAAXAPVVXN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-4268
                                                                   EEKTPLTTAAXAPVVXN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 75.0
Matches 12; Conservative
                    14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: GARY BRETON
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                         US-10-419-128-21327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
US-09-543-681A-4268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Pseud
US-10-419-128-21327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                   δ
                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION UNDER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Nolling, Jork
APPLICANT: Deloughery, Craig
APPLICANT: Deloughery, Craig
APPLICANT: Bush, David
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: PATHO3-04
CURRENT APPLICATION NUMBER: 09/252,991
PRIOR APPLICATION NUMBER: 09/252,991
PRIOR PLILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21327
                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22; Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.8%; Score 63; DB 29; Length 482;
                                                                                                                                                                                                                                                                         Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                       DB 17; L
5.1e-06;
                                                                                                                                                        NAME/KEY: UNSURE
LOCATION: (17)...(17)
OTHER INFORMATION: Inconclusive sequencing data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.8%; Score 63; DB 22 82.4%; Pred. No. 0.057;
                                                                                                                                                                                                                                                                     Ouery Match 93.8%; Score 76; DB Best Local Similarity 100.0%; Pred. No. 5.1 Matches 18; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
US-09-791-537-125872
; Sequence 125872, Application US/09791537
; GENERAL INFORMATION:
                                           LOCATION: (1)...(1)
OTHER INFORMATION: Possibly Ser
NAME/KEY: UNSURE
LOCATION: (12)...(12)
OTHER INFORMATION: Possibly Gly or Ser
      INFORMATION: N-terminal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 21327, Application US/10366683
GENERAL INFORMATION:
APPLICANT: Rubenfield, Marc J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                               2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                           EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 EEKTPLTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||| ||||| ||||| |||| || EEKTRLTTAAGAPUVDN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.0
SEQ ID NO 125872
LENGTH: 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 82.4'
Matches 14; Conservative
                           NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-791-537-125872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-366-683-21327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-366-683-21327
                                                                                                                                                                                                                             US-09-359-426C-2
                                                                                                                                                                                                                                                                            · Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Remaining Prior Application data removed - See File Wrapper or PALM.'
NUMBER OF SEQ ID NOS: 78614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 53; DB 28; Length 495;
Pred. No. 3.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ed. No. 3,5;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 77773, Application US/10282122A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-10-23
                          PRIOR APPLICATION NUMBER: 60/191, 078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-06
PRIOR PELLING DATE: 2000-09-06
PRIOR PELLING DATE: 2000-09-09
PRIOR PELLING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/230, 347
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2001-102-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 75.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 EKKKLTTAAGAPVVDN 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wang, Liangsu
APPLICANT: Zamwdio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haeelbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zyskind, Judith
Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carr, Grant
          CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Proteu
US-10-282-122A-68674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-282-122A-77773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Pates
SEQ ID NO 68674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: Us/09/791,537
CURRENT APPLICATION NUMBER: 201-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 30924
LENGTH: 484
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709-1002-001
CURRENT APPLICATION NUMBER: US/10/603,114
CURRENT FILING DATE: 2003-06-24
PRIOR FILING DATE: 2000-04-05
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
RIOR FILING DATE: 1999-04-09
SEQ ID NOS: 8344
SEQ ID NOS: 8344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22; Length 484;
                                                                                                                                                                                                                                                                                                                                                                                                              DB 31; Length 406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 53;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                              Score 53;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 68674, Application US/10282122A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 30924, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 65.4%;
Best Local Similarity 75.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 EKTPLTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 EKKKLTTAAGAPVVDN 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 EKTPLTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 EKKKLTTAAGAPVVDN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 65.4%;
Best Local Similarity 75.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-791-537-30924
                                                                                                                                                                                                                                                                                                                                  Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, Liangsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamamoto, Re
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trawick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-282-122A-68674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-791-537-30924
                                                                                                                                                                                                                                                                                                                                                            US-10-603-114-4268
                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT
```

셤 ò

g

ò

ó

Gaps

·,

Indels

```
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 16868
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Alakle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERBING: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 45; DB 22; Length 484;
Pred: No. 90;
0; Mismatches 2; Indels
                                                                                                                                          Score 45; DB 29; Length 478;
Pred. No. 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 32; Length 478;
89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                ; LOCATION: (1)..(478)
; OTHER INFORMATION: unsure at all Xaa locations US-10-369-493-13806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (1)..(478)
; OTHER INFORMATION: unsure at all Xaa locations US-60-360-039-13806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                      RESULT 12
US-60-360-039-13806
; Sequence 13806, Application US/60360039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16868, Application US/09791537; GENERAL INFORMATION:
  Pseudomonas fluorescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Pseudomonas fluorescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.6%;
                                                                                                                                            55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 83.3
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 55.6
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                Query Match
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                 7 LTTAAXAPVVXN 18
                                                                                                                                                                                                                                                         1 LTTAAGAPVVDN 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 LTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cao, Yongwei APPLICANT: Chen, Xianf
                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-09-791-537-16868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 13806
                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYPE: PRT
                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261,210
CURRENT PELLING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10(5205.)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOCTWARR: Patentin version 3.1
LENGTH: 480
                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                                                                                                            DB 28; Length 480;
26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.6%; Score 45; DB 22; Length 128; 66.7%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                     Score 48; DB 2
Pred. No. 26;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19306, Application US/09791537 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Streptomyces antibioticus US-09-791-537-19306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                  Query Match 59.3%;
Best Local Similarity 68.8%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          3 EKTPLTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 KKKGLTTAAGAPVVDN 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||| :| || ||||
EEKFDVTAAAAAPVV 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 66.7
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                       ORGANISM: Yersinia pestis
US-10-282-122A-77773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-791-537-19306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEO ID NO 19306
LENGTH: 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 13806
LENGTH: 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                            õ
```

```
Sequence 23365, Application US/09708427
GENERAL INFORMATION:
THE CRIMINATION: ALEXANDROV et al.
TITLE OF INVENTION: THEREBY
FILE REPERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT PILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE PACENTIN Version 3.1
SEQ ID NO 23365
LENGTH: 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-709P
CURRENT APPLICATION NUMBER: US/09/513,996A
CURRENT APPLICATION NUMBER: US/09/513,996A
SURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 81028
SEQ ID NO 35911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 23364, Application US/09708427; GENERAL INFORMATION:
A PAPLICANT: N. ALEXANDROV et al.
TILLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44; DB 21; Length 291;
Pred. No. 72;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.3%; Score 44; DB 19; Length 292;
60.0%; Pred. No. 73;
live 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Location 1..292 / Ceres Seq. ID 1808521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 1..292
OTHER INFORMATION: any n or Xaa = unknown
                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
COCATION: 1..291
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
COCATION: 1..291
UCATION: 1..291
US-09-708-427-233465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 35911, Application US/09513996A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.3%; Scor
60.0%; Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEKAEMTTAMOSPVV 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 EEKAEMTTAMOSPVV 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 60.0 Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 9: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 17
US-09-513-996A-35911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-513-996A-35911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 18
US-09-708-427-23364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 35912, Application US/09513996A
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCODED THEREBY
FILE REPERENCE: 2750-709P
CURRENT APPLICATION NUMBER: US/09/513,996A
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 81028
                                                                                                                                                                                   APPLICANT: La Rosa, Thomas J.
APPLICANT: Ea Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, weiv, Andrey A.
APPLICANT: Wu, weiv, Andrey A.
APPLICANT: Buckharouk, Brad
APPLICANT: Buckharouk, Brad
APPLICANT: Buckharouk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44; DB 30; Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.3%; Score 44; DB 19; Length 291; 60.0%; Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Location 1..291 / Ceres Seq. ID 1808522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT4530_94886C.1.pep
US-10-437-963-199308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 20;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1..291
OTHER INFORMATION: any n or Xaa = unknown
                                                                                                                                                   Sequence 199308, Application US/10437963 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||| :||| :|||
72 EEKAEMTTAMQSPVV 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 EEKTPLTTAAXAP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 EEKTPLVTPQGAP 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 60.0
Matches 9; Conservative
                                    14 LTTAAGAPVVDN 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-09-513-996A-35912
                                                                                                                              US-10-437-963-199308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-513-996A-35912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 199308
LENGTH: 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 35912
LENGTH: 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <sup>'</sup>d
ò
                                    ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
Sequence 35910, Application US/09513996A
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCODED THEREBY
FILE REFERENCE: 2750-709P
CURRENT APPLICATION NUMBER: US/09/513,996A
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 81028
SEQ ID NO 35910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 23363, Application US/09708427

Sequence 23363, Application US/09708427

GENERAL INFORMATION:
APPLICANT: N ALEXANDROV et al.
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: US/09/708,427

CURRENT APPLICATION UNDER: US/09/708,427

CURRENT PILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364

SEQ ID NOS: 85361

LENGTH: 427
                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                    ;
0
                                                                                                                                                                        Score 44; DB 28; Length 306;
Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 44; DB 19; Length 427;
Pred. No. 1.2e+02;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Location 1..427 / Ceres Seq. ID 1808520
US-09-513-996A-35910
                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1..427
OTHER INFORMATION: any n or Xaa = unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature

LOCATION: 1..427

OTHER INFORMATION: Xaa is any amino acid

NAME/KEY: misc_feature

LOCATION: 1..427

COTHER INFORMATION: Ceres Seq. ID 1808520
US-09-708-427-23363
                                                                                                                                                                                                                                                                                              84 EKVPCTSSGVAPIFVNA 100
                                                                                                                                                                                                                                                                3 EKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Arabidopsis thaliana
                                                                                                                                                                          54.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 EEKAEMITAMOSPVV 222
                    version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 EEKTPLTTAAXAPVV 16
                                                                                     TYPE: PRT
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                         8; Conservative
NUMBER OF SEQ ID NOS: 1576
                                                                                                                                                                                           Best Local Similarity
Matches 8, Conserv
                    SOFTWARE: Patentin
SEQ ID NO 1139
                                                                                                                                                                                                                                                                                                                                                                                 RESULT 21
US-09-513-996A-35910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 22
US-09-708-427-23363
                                                                                                                                 US-10-238-075-1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                LENGTH:
                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1135, Application US/10238075
GENERAL INFORMATION:
APPLICANT: I.N.S.E.R.M.
APPLICANT: I.N.S.E.R.M.
TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolar TITLE OF INVENTION: Polynucleotides which are of these polynucleotides and of their FILE REFERENCE: BLANDINE CURRENT APPLICATION NUMBER: US/10/238,075
CURRENT APPLICATION NUMBER: 2002-09-10
PRIOR PILING DATE: 2000-03-10
PRIOR FILING DATE: 2000-03-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Inlemfeldt, Hans-Georg
APPLICANT: Barzu, Octavian
APPLICANT: Barzu, Octavian
APPLICANT: Barzu, Octavian
APPLICANT: Sakamoto, Hiroshi
APPLICANT: Pistocnik, Elisabeth
APPLICANT: Pochet, Philippe
APPLICANT: Pochet, Sylvie
TITLE OF INVENTION: Enzymatic synthesis of deoxyribonucleosides
FILE REFERENCE: 203719WO beoxyribonucleosides
CURRENT PILICATION NUMBER: US/10/049,750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 26; Length 306;
                                                                                                                                                                                                                                                                                                                                                                                                      54.3%; Score 44; DB 21; Length 292; 60.0%; Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.3%; Score 44;
47.1%; Pred. No. 7
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
UNRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: 1..292
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                       ; LOCATION: 1..292
; OTHER INFORMATION: Ceres Seq. ID 1808521
US-09-708-427-23364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION WUMBER: EP99116425.2 PRIOR FILING DATE: 1999-08-20 NUMBER OF SEQ ID NOS: 20 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 12 LENGTH: 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/10049750 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 EKVPCTSSGVAPIFVNA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 EKTPLTTAAXAPVVXNA 19
                                                                                                                                                                               ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||| :||| :||| 73 EEKAEMTTAMQSPVV 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Tischer, Wilhelm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Salmonella typhi
US-10-049-750-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 47.1 Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 20
US-10-238-075-1139
                                                                                                            SEQ ID NO 23364
LENGTH: 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-049-750-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
TITLE OF INVENTION: Blad With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement; FILE REFERENCE: 38-21(53221)B; CURRENT APPLICATION WUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 141172
LENGTH: 373
                                                                                                                                                                                                                                                       APPLICANT: Xu, H.

TITLE OP INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
PRIOR PILING DATE: 2000-03-21
RIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-66
PRIOR PILING DATE: 2000-05-66
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/283,625
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/283,931
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-0-24
PRIOR PILING DATE: 2001-0-12-22
PRIOR PILING DATE: 2001-0-12-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Remaining Prior Application data removed - See File Wrapper or PALM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.3%; Score 44; DB 28; 56.2%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 141172, Application US/10437963 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 RTPLSSTAAAQVVYNA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 47689
LENGTH: 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 KTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
                                                                                                                                                                                             Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 56.2
Matches 9; Conservative
                                                       Ohlsen, Kari
                                                                                                                                                              Carr, Grant
Yamamoto, Rol
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-282-122A-47689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                        APPLICANT: Lutefiyya, Linda L.

TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Transcription In Plants
TITLE OF INVENTION: Transcription In Plants
FILE REFERENCE: 38-21(15300)K
CURRENT APPLICATION NUMBER: US/10/361,942
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: US 60/356,051
PRIOR FILING DATE: 2002-02-11
NUMBER OF SEQ ID NOS: 2906
SEQ ID NO 346
LENGTH: 427
                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Monsanto Technology LLC
APPLICANT: Monsanto Technology LLC
APPLICANT: Lutfiyya, Linda L
TITLE OF INVENTION: WOLZEL ACIDS AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: TRANSCRIPTION IN PLANTS
TILE REPERRORE 38-21 (15300) I
CURRENT APPLICATION WUMBER: US/60/356,051
CURRENT APPLICATION WUMBER: 2002-02-11
NUMBER OF SEQ ID NOS: 2926
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 1468
LENGTH: 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
        Length 427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 427;
                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
  Score 44; DB 21;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.3%; Score 44; DB 29; 60.0%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Clone ID: AT_C7A10.C1.p390.tg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44; DB 32;
Pred. No. 1.2e+02;
                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-282-122A-47689
; Sequence 47689, Application US/10282122A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 24
US-60-356-051-1468
; Sequence 1468, Application US/60356051
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                     US-10-361-942-346; Sequence 346, Application US/10361942; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Arabidopsis thaliana
US-60-356-051-1468
Query Match
Best Local Similarity 60.0%;
Matches 9; Conservative ;
                                                                                                                                           ||| :||| :|||
208 EEKAEMTTAMQSPVV 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 EEKAEMTTAMOSPVV 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 EEKAEMTTAMOSPVV 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 60.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 EEKTPLTTAAXAPVV 16
                                                                                                         2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wang, Liangsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-361-942-346
                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
```

```
APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBI
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 80045, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DAIE: 2000-11-09
NUMBER OF SEQ ID NOS: 83364
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43; DB 22; Length 506;
Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.9%; Score 42; DB 21; Length 120; 50.0%; Pred. No. 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 55;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: 1..120
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature

// LOCATION: 1..120

// OTHER INFORMATION: Ceres Seq. ID 1957331

US-09-708-427-80045
                                                                                                                                               US-09-791-537-92565; Sequence 92565, Application US/09791537; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 80044, Application US/09708427 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Pseudomonas fluorescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 EEKTPVEKKTGVPVVKKA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.1%; 71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S TPLTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 THLTTEAGAPVVDN 24
                  PLTTAAXAPVVXN 18
                                                             5 PLTTEAGAPVADN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 71.4
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-791-537-92565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 30
US-09-708-427-80045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 31
US-09-708-427-80044
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 92565
LENGTH: 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 80045
LENGTH: 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
                    ò
                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
LOGO ID NO 101743
LENGTH: 483
                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.1%; Score 43; DB 27; Length 483; 69.2%; Pred. No. 2e+02; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43; DB 22; Length 483;
Pred. No. 2e+02;
0; Mismatches 4; Indel8
                                                                                                                            Length 373;
                                                                                                                                                                          Indels
                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT4530_42301C.1.pep
US-10-437-963-141172
                                                                                                                          Score 43; DB 30; L. Pred. No. 1.5e+02; 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAL; YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION UNMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR PAPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
                                                                                                                                                                                                                                                                                                                                                                  Sequence 101743, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10589, Application US/10156761
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Streptomyces avermitilis US-10-156-761-10589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Streptomyces violaceus US-09-791-537-101743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.1%;
69.2%;
                                                                                                                               Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
                                                                                                                                                                                                                                                :|:|| |||| |
222 DEETPTTTAARP 234
                                                                                                                                                                                                                   2 EEKTPLTTAAXAP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 PLTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLTTEAGAPVADN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 53.1
Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 53.1
Best Local Similarity 69.2
Matches 9; Conservative
TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                  US-09-791-537-101743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-156-761-10589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 10589
LENGTH: 483
                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                            a
```

ö

Gaps

ö

```
US-09-513-996A-54519

Sequence 54519, Application US/09513996A

Sequence 54519, Application US/09513996A

GENERAL INFORMATION:

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: ENCODED THEREBY

TITLE OF INVENTION: ENCODED THEREBY

FILE REFERENCE: 2750-709P

CURRENT APPLICATION NUMBER: US/09/513,996A

CURRENT FILING DATE: 2000-02-25

NUMBER OF SEQ ID NOS: 81028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 27614, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85564
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                     Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42; DB 19; Length 172; Pred. No. 86; B; Indels 1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ID 2109050
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB 21;
Pred. No. 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Location 1..172 / Ceres Seq. US-09-513-996A-54519
                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: any n or Xaa = unknown
                                                                                                                                                                             NAME/KEY: misc_feature
| COCATION: 1..161
| OTHER INFORMATION: Xaa is any amino acid
| OTHER INFORMATION: Xaa is any amino acid
| NAME/KEY: misc_feature
| LOCATION: 1..161
| OTHER INFORMATION: Ceres Seq. ID 1821333
US-09-708-427-27615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 EEKTPVEKKTGVPVVKKA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 EEKTPVEKKTGVPVVKKA 148
  2000-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 EEKTPLTTAAXAPVVXNA 19
                                                                                                               TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                       51.9%;
                     NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 27615
LENGTH: 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 51.9%;
Best Local Similarity 50.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
  CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-708-427-27614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 54519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 27614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: N. ALEXADICATION:
APPLICANT: N. ALEXADICAN: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REPERENCE: 2750-1243P
CURRENT APPLICADION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NOS: 85364
SEQ ID NOS: 85364
LENGTH: 147
         TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY FILE REPRENCE: 2750-1243P CURRENT APPLICATION VUMBER: US/09/708,427 CURRENT FILING DATE: 2000-11-09 NUMBER OF SEQ ID NOS: 85364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 27615, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REPERBNCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21; Length 147; 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.9%; Score 42; DB 21; Length 138, 50.0%; Pred. No. 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 2
Pred. No. 71;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc feature
LOCATION: 1..138
OTHER INFORMATION: Ceres Seq. ID 1957330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature

) LOCATION: 1..147

SOTHER INFORMATION: Ceres Seq. ID 1957329

US-09-708-427-80043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1..147
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 EEKTPVEKKTGVPVVKKA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 EEKTPVEKKTGVPVVKKA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                   ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.0%;
Matches 9; Conservative
APPLICANT: N. ALEXANDROV et al
                                                                                                                                                             SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 50.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature LOCATION: 1..138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-708-427-80044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 32
US-09-708-427-80043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-708-427-27615
                                                                                                                                                                             SEQ ID NO 80044
LENGTH: 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
```

ö

Gaps

ö

```
APPLICANT: Cao, Yongwei Through Molecules and Other Molecules Associated With TITLE OF INVENTION: Wallet and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313)B CURRENT APPLICATION WUBER: US/10/425,114

CURRENT APPLICATION DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                        ô
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REPERENCE: 38-10 (22726) C
CURRENT APPLICATION NUMBER: US/10/219, 999
CURRENT FILING DATE: 2002-08-15
PRIOR FILING DATE: 2001-09-21
PRIOR PLING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 60/312,544
PRIOR APPLICATION NUMBER: US 60/312,544
PRIOR PILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 63520
SEQ ID NO 51870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42; DB 28; Length 322;
Pred. No. 1.9e+02;
1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.9%; Score 42; DB 30; Length 322;
50.0%; Pred. No. 1.9e+02;
tive 1; Mismatches 8; Indels
                                           Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: LIB3180-051-E8_FLI.pep
US-10-425-114-63257
                                        Score 42; DB 21;
Pred. No. 1.9e+02;
1; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 63257, Application US/10425114
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
                                                                                                                                                                                                                                                                          US-10-219-999-51870
; Sequence 51870, Application US/10219999
; GENERAL INFORMATION:
                                                                                                                                                                 |||||:
291 EEKTPVEKKTGVPVVKKA 308
                                                                                                                                      2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 EEPTPAATAAASPAPDRA 61
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cao, Yongwei
APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Kovalic, David K.
                                           51.9%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 50.0
Matches 9; Conservative
                                                                                        Conservative
                     Query Match
Best Local Similarity
Local 9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Zea mays
US-10-219-999-51870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 39
US-10-425-114-63257
US-09-708-427-27613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 63257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                  RESULT 38
                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 36
US-09-513-996A-54518
Squence 54518, Application US/09513996A
Squence 54518, Application US/09513996A
Squence 54518, Application US/09513996A
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCODED THEREBY
TITLE OF INVENTION: ENCODED THEREBY
TITLE OF INVENTION: ENCODED THEREBY
CURRENT APPLICATION NUMBER: US/09/513,996A
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 81028
SEQ ID NO 54518
LENGTH: 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 27(513, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDON et al.
APPLICANT: N. ALEXANDON et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85564
SOFTWARE: PALENTIN version 3.1
SEQ ID NO 27613
                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                         Query Match 51.9%; Score 42; DB 21; Length 204; Best Local Similarity 50.0%; Pred. No. 1.1e+02; Matches 9; Conservative 1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 51.9%; Score 42; DB 19; Length 215; Best Local Similarity 50.0%; Pred. No. 1.1e+02; Matches 9; Conservative 1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Location 1..215 / Ceres Seq. ID 2109049
US-09-513-996A-54518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: UNSURE
LOCATION: 1..215
OTHER INFORMATION: any n or Xaa = unknown
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..204
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..204
OTHER INFORMATION: Ceres Seq. ID 1821332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: 1..321
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: 1..321
OTHER INFORMATION: Ceres Seq. ID 1821331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 EEKTPVEKKTGVPVVKKA 191
                                                                                                                                                                                                                                                                                                                                                  174 EEKTPVEKKTGVPVVKKA 191
                                                                                                                                                                                                                                                                                                       2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Arabidopsis thaliana
                                                                                                                                                                 US-09-708-427-27614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-708-427-27613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ે
                                                                                                                                                                                                                                                                                                          ઠે
```

```
Sequence 54517, Application US/09513996A

GENERAL INFORMATION:
APPLICAMTON:
APPLICAMTON:
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCODED THEREBY
FILE REFERENCE: 2750-709P
CURRENT APPLICATION NUMBER: US/09/513,996A
CURRENT PILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 81028
SEQ ID NOS 4517
LENGTH: 332
TYPE: PRT
CORGANISM: Arabidopsis thaliana
FEATURE:
COATION: 1..332
COATION: 1..332
COATION: LOCATION: Location 1..332 / Ceres Seq. ID 2109048
US-09-513-996A-54517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 51.9%; Score 42; DB 19; Length 332; Best Local Similarity 50.0%; Pred. No. 1.9e+02; Matches 9; Conservative 1; Mismatches 8; Indels
2 EEKTPLTTAAXAPVVXNA 19
                                     RESULT 40
US-09-513-996A-54517
           ò
                                                   g
```

.; 0

Gaps ; 0

-Search completed: January 28, 2004, 13:14:54 Job time : 172 secs

|||||: 291 EEKTPVEKKTGVPVVKKA 308 2 EEKTPLTTAAXAPVVXNA 19

ģ

(DIASIN ANNE IN THE SHAPE OF TH

Н

```
Sequence 27570, Application US/09614150A
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUC
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
CURRENT APPLICATION NUMBER: US/09/614,150A
CURRENT FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 63257, A
Sequence 27570, A
Sequence 30864, A
Sequence 5631, Ap
Sequence 29, Appl
Sequence 29, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64721, A
611, App
3, Appli
59823, A
39997, A
19753, A
7671, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68517, A
46588, A
41325, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7762, Ap
21767, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16, Appl
30690, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23185,
                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                January 28, 2004, 13:08:39 ; Search time 22 Seconds (without alignments) 64.984 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                        Pending_Patents_AA_New:*

1: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USO7_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/USO9_NEW_COMB.pep:*
5.1.6
Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US03-10308A-29
US-10-406-668A-29
US-10-679-063-21762
US-10-679-063-21767
US-60-470-220-16
US-09-614-150A-3059
US-10-425-114A-4658B
US-10-425-114A-4658B
US-10-425-114A-4658B
US-10-425-114A-4658B
US-10-425-114A-4658B
US-10-425-114A-5923
US-10-425-114A-39997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S-10-415-182A-6506
S-09-323-998E-57
S-09-323-998E-58
S-09-323-998E-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -10-425-114A-39997
-10-679-063-19753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-614-150A-8541
US-09-614-150A-30864
US-09-614-150A-5631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-679-063-23185
                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                             364858 segs, 75244621 residues
version 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                            - protein search, using sw model
                                                                                                                                      1 XEEKTPLTTAAXAPVVXNA 19
                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
GenCore (c) 1993
                                                                                                                                                                                                                                          length: 0
length: 2000000000
                                                                                                           US-09-359-426C-2
81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       322
1012
788
1473
1793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1162
19695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3304
3324
3396
3396
500
500
500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164
         Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4446.9
4446.9
446.9
446.9
446.9
475.7
475.7
                                                                                                                                                                                                                                                                                                                                       .........
                                                                                                                                                                                                                                              sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39
39
39
39
39
39
39
39
39
39
                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                          Minimum DB Maximum DB
                                            OM protein
                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                      Sequence:
                                                                                                                                                                                                Searched:
                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
```

```
APPLICANT: Except, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114A
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 63257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                       22, Appl
39876, A
864, App
                                                                                                                                                                                                                                     55, Appl
                                                                                                                                                                               70539,
                                                                                                                               14309,
                                                                                                                                                                                                                       43398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
              Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                        Sequence
Sequence
Sequence
                                                                                                                             Sequence
Sequence
                                                                                                                                                       Sequence
                                                                                                                                                                                                          Sequence
                                                                                                                                                                                  Sequence
                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3180-051-E8_FLI.pep
US-10-425-114A-63257
US-09-614-150A-17034
US-10-425-114A-65245
US-09-614-150A-18177
PCT-US03-38193-3242
US-10-702-386-3342
US-10-70-439-142
US-60-519-270-229
US-10-719-547-22
US-09-614-150A-9876
US-09-614-150A-9876
US-10-79-930-9369
US-10-425-114A-52153
US-10-425-114A-66503
US-10-425-114A-66503
US-10-425-114A-66503
US-10-425-114A-66503
US-10-425-114A-66503
US-10-425-114A-66503
US-10-425-114A-66503
US-10-425-114A-66503
US-10-425-114A-66503
US-10-679-663-19265
US-10-679-663-19265
US-10-679-663-19265
US-10-679-663-19265
US-10-679-663-19265
US-10-679-663-19265
US-10-679-663-19265
US-10-679-663-19265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42; DB 6
Pred. No. 16;
1; Mismatches
                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                          US-10-425-114A-63257
; Sequence 63257, Application US/10425114A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            || || || || || 14 EEPTPAATAAASPAPDRA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.9%;
                                                                                                                                                                                                                                                                                                                                                                             Zhou, Yihua
Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 50.0
Matches 9; Conservative
  630
11064
110664
13390
208
208
208
3114
310
310
486
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Zea mays
  44.4
44.4
                                                                                                                                                        44.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-614-150A-27570
```

NUCLEIC ACID EXPRESSION OF 10,000 OR MORE

```
APPLICANIS DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
CURRENT FILING DATE: 2000-07-11
CURRENT FILING DATE: 1999-10-05
PRIOR PAPLICATION NUMBER: 60/160,191
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR PILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-11-12
PRIOR PILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR PILING DATE: 1000-01-12
PRIOR PILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-01-12
PRIOR PILING DATE: 1999-11-2
PRIOR PILING DATE: 1999-11-2
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR PILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-01-12
PRIOR PAPLICATION NUMBER: 60/191,637
                                                                                                                                                            APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CLO00728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB 5; Lu
Pred. No. 1.8e+02;
2; Mismatches 5;
                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/614,150A CURRENT PELING DATE: 2000-07-11 PRIOR PAPELICATION NUMBER: US/157,832 PRIOR PAPELICATION NUMBER: G0/157,832 PRIOR PILING DATE: 1999-10-05 PRIOR APPLICATION NUMBER: G0/160,191 PRIOR PILING DATE: 1999-10-19 PRIOR PILING DATE: 1999-10-28 PRIOR PILING DATE: 1999-10-28 PRIOR PILING DATE: 1999-11-12 PRIOR APPLICATION NUMBER: G0/164,769 PRIOR PILING DATE: 1999-12-28 PRIOR PILING DATE: 1999-12-28 PRIOR PILING DATE: 2000-02-24 PRIOR PILING DATE: 2000-02-24 PRIOR PILING DATE: 2000-03-23 PRIOR PILING DATE: 2000-03-23 PRIOR PILING DATE: 2000-03-24 PRIOR PILING DATE: 2000-03-24 PRIOR PILING DATE: 2000-03-24 PRIOR PILING DATE: 2000-03-24 PRIOR PILING DATE: 2000-03-23 NUMBER OF SEQ ID NOS: 43008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5631, Application US/09614150A
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1315 DEQAPYTEAALGPVV 1329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49.4%;
ilarity 53.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 8; Conserv
                                                                               Sequence 30864, Appl
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-614-150A-30864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-614-150A-5631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 30864
LENGTH: 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: et al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

FILE REFERENCE: CL00728

CURRENT APPLICATION NUMBER: US/09/614,150A

CURRENT FILING DATE: 2000-07-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 5; Length 1012;
Pred. No. 82;
2; Mismatches 5; Indels '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49.4%; Score 40; DB 5; Length 788; 52.9%; Pred. No. 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/157, 832
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-19
PRIOR PILING DATE: 1999-10-19
PRIOR PILING DATE: 1999-10-19
PRIOR PILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR PILING DATE: 1999-11-12
PRIOR PELING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-28
PRIOR FILING DATE: 1999-11-28
PRIOR FILING DATE: 1999-11-28
PRIOR FILING DATE: 1999-11-28
PRIOR FILING DATE: 2000-01-12
PRIOR PELING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
NUMBER OF SEQ ID NOS: 43008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 92;
1; Mismatches
                 PRIOR FILING DATE: 1999-10-28
PRIOR PLING DATE: 1999-10-28
PRIOR PLING DATE: 1999-11-12
PRIOR PLING DATE: 1999-11-12
PRIOR PLING DATE: 1999-11-28
PRIOR FLING DATE: 1999-11-28
PRIOR FLING DATE: 1999-11-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR PLING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FLING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FREESEQ FOR WINGOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 50.6%; Score 41; Best Local Similarity 53.3%; Pred. No. Matches 8; Conservative 2; Mismatcl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8541, Application US/09614150A GENERAL INFORMATION:
60/161,932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       602 EDGPTTTAAAAPLASAA 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 EKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           695 EEVTPYNTAPHSPIV 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Venter, J. Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: DROSOPHILA
US-09-614-150A-27570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DROSOPHILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-614-150A-8541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-614-150A-8541
                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 27570
LENGTH: 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFIMAL
SEQ ID NO 8541
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
```

Gaps

Length 1473; Indels

```
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT CORGANISM: Streptomyces avermitilis MA-4680 US-10-679-063-21767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-679-063-21767; Sequence 21767, Application US/10679063; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | |||||||| :: |
189 EITPLTTAALVDLLVEA 205
                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas sp. CF600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 EETPLTTALLGEVMQAA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 EKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 EKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Conservative
  7 LTTAAXAPVVXN 18
                                         13 LTNAAGAPIVEN 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity
Matches 9; Conserv
                                                                                                                   US-10-679-063-7762
                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-679-063-7762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 21767
LENGTH: 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
US-60-470-920-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                             LENGTH: 486
                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
  ò
                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                   ä
                                                                                                                                                                          Length 1793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39; DB 1; Length 484;
Pred. No. 81;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6; Length 484;
                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: CROOKE, HELEN RACHEL
APPLICANT: SHEA, JACQUELINE ELIZABETH
APPLICANT: FELDMAN, ROBERT GRAHAM
APPLICANT: COUTEBROZE, SYLVAIN GABRIEL
APPLICANT: COUTEBROZE, SYLVAIN GABRIEL
APPLICANT: AFFLICANT: AFFRUATED
TITLE OF INVENTION: ATTENUATED GRAM NEGATIVE BACTERIA
FILE REFERENCE: 454313-3171.1
CURRENT APPLICATION NUMBER: US/10/406,686A
CURRENT FILING DATE: 2003-04-03
PRIOR APPLICATION NUMBER: 60/370,282
PRIOR APPLICATION NUMBER: 60/370,282
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MENTALL LIMITED
TITLE OF INVENTION: ATTENUATED GRAM NEGATIVE BACTERIA
FILE REPERENCE: 454313-3171.MO
CURRENT APPLICATION NUMBER: PCT/US03/10308A
CURRENT FILING DATE: 2003-08-19
PRIOR APPLICATION NUMBER: 60/370,282
PRIOR PLILING DATE: 2002-04-05
NUMBER: PALENT OF SERVICE OF SERVICE OF SERVING DATE: 2002-04-05
NUMBER: PALENT OF SERVICE OF SERVING DATE: 201
SOFTWARE: PALENT OF SERVING DATE: 2.1
TYPE: PRIOR PLILING DATE: 2.1
TYPE: PRIOR PRIOR DATE: 2.1
                                                                                                                                                                        Score 39.5; DB 5;
Pred. No. 2.7e+02;
3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

48.1%; Score 39; DB

Best Local Similarity 66.7%; Pred. No. 81;

Matches 8; Conservative 1; Mismatches
                                                                                                                                                                                                                 3; Mismatches
                NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5631
LENGTH: 1793
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 29, Application PC/TUS0310308A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-406-686A-29; Sequence 29, Application US/10406686A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                               2 EEKTPLTT-AAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            i LENGTH: 484
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-10-406-686A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Pasteurella multocida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.18;
                                                                                                                                                                        Query Match
Best Local Similarity 52.6%;
Matches 10; Conservative
PRIOR FILING DATE: 2000-03-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 LTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         || || || || 1
13 LTNAAGAPIVEN 24
                                                                                                              ORGANISM: DROSOPHILA
                                                                                                                                   US-09-614-150A-5631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US03-10308A-29
                                                                                                                                                                                                                                                                                                                                                                           PCT-US03-10308A-29
                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                          ò
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
Sequence 7762, Application US/10679063
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
Michael APPLICANT: Edgerton, Michael DIANTS WITH IMPROVED PHENOTYPES TITLE OF INVENTION: TRANSCENIC PLANTS WITH IMPROVED PHENOTYPES FILE REPERENCE: 38-15 (52054) B
CURRENT APPLICATION NUMBER: 2003-10-02
PRIOR APPLICATION NUMBER: 60/415,758
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
SEQ ID NO 7762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52054)8
CURRENT APPLICATION NUMBER: US/10/679,063
CURRENT FILING DATE: 2003-10-02
PRIOR PEDLICATION NUMBER: 60/415,758
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39; DB 6; Length 486;
Pred. No. 82;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.1%; Score 39; DB 6; Length 509; 52.9%; Pred, No. 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16, Application US/60470920
GENERAL INFORMATION:
APPLICANT: Luke, Catherine, J.
APPLICANT: Vialta, Adrian
APPLICANT: Wloch, Mary K.
APPLICANT: Wloch, Mary K.
APPLICANT: Geall, Andrew J.
TITLE OF INVENTION: DNA INFluenza Vaccine Compositions
FILE REFERENCE: 1530.0640000
CURRENT APPLICATION NUMBER: US/60/470,920
CURRENT FILING DATE: 2003-05-16
NUMBER OF SEQ ID NOS: 45
```

ö

ö

```
Query Match
Best Local Similarity 63...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 :|||||: :||
104 SPLTTASLSPV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 SPLTTASLSPV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 TPLTTAAXAPV 15
                                                                                                                                                                                                                                                                                                                                                                                   5 TPLTTAAXAPV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
US-10-425-114A-46588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-09-614-150A-41325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 46588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: et al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

FILE REFERENCE: CLOOO728

CURRENT APPLICATION NUMBER: US/09/614,150A

CURRENT FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: 60/150,191

PRIOR APPLICATION NUMBER: 60/160,191

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR APPLICATION NUMBER: 60/173,383

PRIOR FILING DATE: 1999-10-28

PRIOR APPLICATION NUMBER: 60/173,693

PRIOR APPLICATION NUMBER: 60/175,693

PRIOR PLING DATE: 1999-10-12

PRIOR PLING DATE: 2000-01-12

PRIOR PLING DATE: 2000-01-12

PRIOR PLING DATE: 2000-03-23

NUMBER: 60/191,637

PRIOR FILING DATE: 2000-03-23

NUMBER: FSECTED NOS: 43008

SOFTWARE: FSECTED CONTINUENT NUMBER: 60/191,637

PRIOR FILING DATE: 2000-03-23

NUMBER: FSECTED NOS: 43008

SEQ ID NO 30690

LEGISTH: 842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38.5; DB 5; Length 842;
Pred. No. 1.8e+02;
                                                                                                                                                                Score 39; DB 7; Length 560;
Pred. No. 95;
3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 30690, Application US/09614150A GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 68517, Application US/10425114A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  598 EKTPIYSTTTKAPVVSTS 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 EKTPL-TTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                     2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                               19 EELTPGTSGATRPIIKPA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.5%;
SOFTWARE: PatentIn version 3.2
SEQ ID NO 16
LENGTH: 560
                                                                                                                                                                        Query Match
Best Local Similarity 44.4%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Seeven E
APPLICANT: Screen, Seeven E
APPLICANT: Tabaska, Jack E
                                                                                       ; ORGANISM: Influenza B virus US-60-470-920-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.0
Matches. 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: DROSOPHILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-614-150A-30690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-425-114A-68517
                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-614-150A-30690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                  셤
```

```
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Ebou, Yihua
APPLICANT: Sou, Yihua
APPLICANT: Soreen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Coo, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21(53313)B
CURRENT PAPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CL000728
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 186;
                                                                                                                                                                                , OTHER INFORMATION: Clone ID: UC-ZMROTEOSINTE016B01_FLI.pep US-10-425-114A-68517
                                                                                                                                                                                                                                                                        Length 116
                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6;
44;
                                                                                                                                                                                                                                                                      DB. 6;
.26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: 700427386_FLI.pep
US-10-425-114A-46588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT PEDILCATION NUMBER: US/09/614,150A
CURRENT FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR PILING DATE: 1999-10-19
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR APPLICATION NUMBER: 60/164,769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
CURRENT APPLICATION NUMBER: US/10/425,114A CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 73128 SEQ ID NO 68517 LENGTH: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38;
Pred. No.
                                                                                                                                                                                                                                                                        Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 41325, Application US/09614150A GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 46588, Application US/10425114A GENERAL INFORMATION:
                                                                                                                         TYPE: PRT
ORGANISM: Zea mays subsp. mexicana
                                                                                                                                                                                                                                                                        46.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.9%;
```

```
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 18
US-10-425-114A-59823
                                                                                                         US-60-490-890-611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 59823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-084-846A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 164
                      SEQ ID NO 611
                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dp
                                                                                                                                                                                                                                        Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Zhou, Yihua Zhou, Yihua Zhou'd K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen. Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Value and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rupnow, Brent A.
APPLICANT: Webster, Kevin R.
APPLICANT: Jackson, Donald
APPLICANT: Wong, Tai W.
TITLE OF INVENTION: BIOMARKERS OF CYCLIN-DEPENDENT KINASE MODULATION
FILE REFERENCE: D0310 PSP
                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 6; Length 229;
                                                                                                                                                                                                                                                                                                                                                                 DB 5; Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Clone ID: LIB4605-005-B1_FLI.pep
                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
               PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: PSESEQ for Windows Version 4.0
SEQ ID NO 41325
LENGTH: 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 46.9%; Score 38; Best Local Similarity 47.1%; Pred, No. ! Matches 8; Conservative 2; Mismatch
                                                                                                                                                                                                                                                                                                                                                                 Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/60/490,890
CURRENT FILING DATE: 2003-07-29
NUMBER OF SEQ ID NOS: 2779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 64721, Application US/10425114A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 611, Application US/60490890
GENERAL INFORMATION:
APPLICANT: Li, Martha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 EEKTPLTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EETPPLLAAAGSPVTAS 17
                                                                                                                                                                                                                                                                                                                                                                 46.9%;
58.3%;
PRIOR FILING DATE: 1999-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 TPVTPAPTAPVI 212
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 TPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                ORGANISM: DROSOPHILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                         US-09-614-150A-41325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-425-114A-64721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-10-425-114A-64721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 64721
LENGTH: 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-60-490-890-611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
```

```
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION WUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Protein 1: amino acid sequence encoded by coding strand 1. OTHER INFORMATION: Start codon: gga, Start position: nucleotide 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38; DB 6; Length 19695;
Pred. No. 6e+03;
                                                                         46.9%; Score 38; DB 7; Length 1162; 46.7%; Pred. No. 3e+02;
                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MULLENWEG, AGNES
APPLICANT: TREFZER, AXEL
APPLICANT: BECHTHOLD, ANDREAS
TITLE OF INVENTION: AVILLAMYCIN DERIVATIVES
FILE REFERENCE: 1974-005
CURRENT APPLICATION UNMBER: US/10/084,846A
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: PCT/EP01/09815
PRIOR APPLICATION NUMBER: DE 101 09 166.4
PRIOR PILING DATE: 2001-08-24
PRIOR PILING DATE: 2001-02-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Streptomyces viridochromogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 59823, Application US/10425114A GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                              RESULT 17
US-10-084-946A-3
iSequence 3, Application US/10084846A
iGENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.9%;
                                                                                                                                                                                                                                                                                                                                                                                              GABRIELE
                                                                                                                                                                                                        ||: || :|: |
550 TPVRPAAASPIVSGA 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhou, Yihua
Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
                                                                                                                                                                       5 TPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             || :| | || :
15780 TPASTRAAAPVI 15791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 120
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 3
LENGTH: 19695
                                                                                                Best Local Similarity 46.7
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 TPLTTAAXAPVV 16
ORGANISM: Homo sapiens
```

```
RESULT 22

10.10-415-182A-6506

10.8-10-415-182A-6506, Application US/10415182A

10.9-10-415-182A

10.9-10-415-182A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 57, Application US/09323998E GENERAL INFORMATION:
APPLICANT: CUNNINGHAM JR., FRANCIS X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Streptococcus agalactiae US-10-415-182A-6506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.7%;
40.0%;
                                                                                                                                                                                                                                                                                                                                       45.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 EQKYPLVSALSRPII 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 ORKAPATTAAALP 49
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      2 EEKTPLTTAAXAP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                          ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 23
US-09-323-998E-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 6506
                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                             LENGTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Сp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                      Other Molecules Associated With
                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                              APPLICANT: Zhou, Yihua APPLICANT: Zhou, Yihua APPLICANT: Zhou, Yihua APPLICANT: Zhou, Yihua APPLICANT: Kovalic, David K. APPLICANT: Screen, Steven E APPLICANT: Tabaska, Jack E APPLICANT: Tabaska, Jack E APPLICANT: Tabaska, Jack E TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Asset TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Asset TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFRENCE: 38-21(53313)B CURRENT APPLICATION NUMBER: US/10/425,114A CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
0
                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REPERBERS: 38-15(52054)8
CURRENT APPLICATION NUMBER: US/10/679,063
CURRENT FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: 60/415,758
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
                                                         Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Length 229;
                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
, OTHER INFORMATION: Clone ID: LIB3912-049-F8_FLI.pep
US-10-425-114A-59823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.7%; Score 37; DB 6; Le 50.0%; Pred. No. 1.1e+02; tive 2; Mismatches 5;
                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEATURE:
OTHER INFORMATION: Clone ID: 700945759_FLI.pep
                                               DB 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB (
Pred. No. 80;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: Bradyrhizobium japonicum USDA 110
US-10-679-063-19753
                                                       Score 37;
Pred. No.
                                                                                                                                                                                                                                                              Sequence 39997, Application US/10425114A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19753, Application US/10679063 GENERAL INFORMATION:
                                                     45.7%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 46.2%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :|||:||:
194 KEKGPMTTSTASP 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 TPLTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 EEKTPLTTAAXAP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match . 45.7
Best Local Similarity 50.0
Matches 7; Conservative
                                                       Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                    5 TPLTTAAXAP 14
                                                                                                                                                                       30 rPSTTAAPAP 39
                                                                                                                                                                                                                                                                                                          APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Glycine max
                                                                                                                                                                                                                                                  US-10-425-114A-39997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-425-114A-39997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-679-063-19753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 39997
LENGTH: 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 19753
LENGTH: 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
```

106 TPĽWVÁIAÁPLIGN 119

RESULT 21

```
Sequence 7771, Application US/1073930

ABBEDTANIAN DOMAIN DOWAIG THE CAID WOLKEULES AND OTHER WOLKCULES ASSOCIATED WITH ITLE OF INNERTON PRICE CAID WOLKER ASSOCIATED WITH ITLE OF INNERTON PRICES AND USES THEREOF FOR PLANT INPROVEMENT ITLE OF INNERTON PRICES AND USES THEREOF FOR PLANT INPROVEMENT STATES AND USES THE FOR THE FAT OFFICE AND THE F
```

ö

ð g

```
APPLICANT: et al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

TITLE OF INVENTION: ADSOPHILA GENES.

PILE REFERENCE: CL000728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                ö
                                                                                                                                                                                                                                           Sequence 23.165, Application US/10679063
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52054)B
CURRENT APPLICATION UNMBER: US/10/679,063
CURRENT FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: 60/415,758
PRIOR APPLICATION NUMBER: 60/415,758
NUMBER OF SEQ ID NOS: 27373
SEQ ID NO 22185
Score 37; DB 5; Length 500;
Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.7%; Score 37; DB 5; Length 630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB 6; Length 564
Pred. No. 2.1e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Oryza sativa (japonica cultivar-group)
US-10-679-063-23185
                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/614,150A CURRENT FILING DATE: 2000-07-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17034, Application US/09614150A GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/157,832
PRIOR PILING DATE: 1999-10-05
PRIOR PEDICATION NUMBER: 60/160,191
PRIOR PELING DATE: 1999-10-19
PRIOR FLING DATE: 1999-10-19
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-11-12
PRIOR PILING DATE: 1999-11-12
PRIOR PILING DATE: 1999-11-12
PRIOR PILING DATE: 1999-11-12
PRIOR PILING DATE: 1999-12-8
PRIOR PILING DATE: 1999-12-8
PRIOR PILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 2000-03-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 66.7
Matches 8; Conservative
                                             8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 TTAAXAPVVXNA 19
                                                                                                                                 372 TLAAAPVVANA 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 TTSAAAPVVVEA 70
                                                                                         9 TAAXAPVVXNA 19
                   Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-614-150A-17034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-614-150A-17034
                                                                                                                                                                                                       RESULT 26
US-10-679-063-23185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM:
  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  П
                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-32-998E-58
Sequence 58, Application US/09323998E
GENERAL INFORMATION:
THEORY THORMATION:
TITLE OF INVENTION: GENES OF CAROTENOLD BIOSYNTHESIS AND METABOLISM AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 108172-09019
CURRENT APPLICATION NUMBER: US/09/323,998E
CURRENT FILING DATE: 1999-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR PELICATION NUMBER: 09/088,724
PRIOR PLICATION NUMBER: 09/088,725
PRIOR PELING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 09/088,725
PRIOR SEQ ID NOS: 62
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 58
LENGTH: 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 25
US-09-323-998E-59
i Sequence 59, Application US/09323998E
j General Tribuston:
APPLICANT: CUNNINGHAM JR., FRANCIS X.
APPLICANT: CUNNINGHAM JR., FRANCIS X.
TITLE OF INVENTION: METHOS OF CAROTENOID BIOSYNTHESIS AND METABOLISM AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 108172-09019
CURRENT APPLICATION NUMBER: US/09/323,998E
CURRENT FILING DATE: 1999-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
NUMBER OF SEQ ID NOS: 62
NUMBER OF SEQ ID NOS: 62
SOFTHARRE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                          Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37; DB 5; Length 500; Pred. No. 1.8e+02; 0; Mismatches 3; Indels
                                                                                                                                                                                                     Score 37; DB 5; Length 498
Pred. No. 1.8e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.78;
                                                                                                                                                                                                       Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
              NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 57
LENGTH: 498
TYPE: PRT
ORGANISM: Capsicum annuum
PRIOR FILING DATE: 1998-06-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                           370 TLAAAPVVANA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             372 TLAAAPVVANA 382
                                                                                                                                                                                                                                                                                                   9 TAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 TAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-323-998E-58
                                                                                                                                                         US-09-323-998E-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-323-998E-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 59
LENGTH: 500
```

a

ઠે

ö

```
RESULT 30
FORTURE 318193-3242
FORTURE 3242, Application PC/TUS0338193
FORTURE 3242, Application PC/TUS0338193
FORTURE 3242, Application PC/TUS0338193
FORTURE 3242, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Ginsburg, Wendy M.
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma, Compositions FILE REFERENCE: 05882.0193 00000
CURRENT APPLICATION NUMBER: PCT/US03/38193
CURRENT FILING DATE: 2003-11-26
FRIGH APPLICATION NUMBER: 60429,739
FRIGH APPLICATION NUMBER: 60429,739
FRIGH APPLICATION NUMBER: 60429,739
FRIGH APPLICATION NUMBER: 60429,739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 1; Length 1064;
Pred. No. 4.1e+02;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1064;
                                                                                      Length 865;
                                                                                    Query Match
45.7%; Score 37; DB 5; Length 865
Best Local Similarity 53.3%; Pred. No. 3.3e+02;
Matches 8; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 6; Le
Pred. No. 4.1e+02;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3242, Application US/10723860 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 8393
SOFTWARE: Patentin version 3.2
SEQ ID NO 3242
LENGTH: 1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.2 SEQ ID NO 3242
                                                                                                                                                                                                                                    102 KDAŤPAŤTÁAPLPPV 116
                                                                                                                                                                                       2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1048 ESSTPGTTAASMP 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1048 ESSTPGTTÄÄSMP 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 61.5-
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 61.5.
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 EEKTPLTTAAXAP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 EEKTPLTTAAXAP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 8393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM:, Homo sapiens
US-10-723-860-3242
                      DROSOPHILA
                   ; ORGANISM: DROSOPI
US-09-614-150A-18177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US03-38193-3242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 31
US-10-723-860-3242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1064
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠ
                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                 APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Con Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: NUMBER: US/10/425, 114A
CURRENT APPLICATION NUMBER: US/10/425, 114A
                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEIC ACID
EXPRESSION OF 10,000 OR MORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 715;
                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: LIB4745-009-A8_FLI.pep US-10-425-114A-65245
  Pred. No. 2.3e+02;
5; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37; DB 6; I
Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCTITLE OF INVENTION: DETECTION KIT, SUCH AS NUCTITLE OF INVENTION: DEROSPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CLOOD.28

CURRENT APPLICATION NUMBER: US/09/614,150A

CURRENT FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: 60/157,832

PRIOR APPLICATION NUMBER: 60/161,932

PRIOR PILING DATE: 1999-10-28

PRIOR PILING DATE: 1999-10-28

PRIOR PILING DATE: 1999-10-28

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR PILING DATE: 1999-11-2

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR APPLICATION NUMBER: 60/175,693

PRIOR APPLICATION NUMBER: 60/175,693

PRIOR PILING DATE: 1999-12-28

PRIOR APPLICATION NUMBER: 60/175,693

PRIOR PILING DATE: 1099-12-28

PRIOR APPLICATION NUMBER: 60/175,693

PRIOR APPLICATION NUMBER: 60/184,831

PRIOR APPLICATION NUMBER: 60/191,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                       Sequence 65245, Application US/10425114A
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18177, Application US/09614150A GENERAL INFORMATION:
                        5
                                                                                                     :||:| : ||| ::
235 QTPMTVSRAAPVASDS 250
                                                                        4 KTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.7%;
ilarity 61.5%;
Conservative
  Best Local Similarity 37.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 PLTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 PLCTDARAPVLLN 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Venter, J. Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Zea mays
                                                                                                                                                                                            RESULT 28
US-10-425-114A-65245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-614-150A-18177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 65245
LENGTH: 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                    셤
                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

ó;

Gaps

ö

Gaps

```
Sequence 39976, Application US/09614150A

Sequence 39976, Application US/09614150A

GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: Venter, J. Craig

APPLICANT: Venter, J. Craig

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DETECTION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
CURRENT FILING DATE: 1090-10-05

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-19

PRIOR FILING DATE: 1999-10-19

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 1999-11-28

PRIOR FILING DATE: 1999-12-28

PRIOR FILING DATE: 1999-12-28

PRIOR FILING DATE: 1999-11-2

PRIOR FILING DATE: 2000-01-12

PRIOR FILING DATE: 2000-01-12

PRIOR FILING DATE: 2000-01-24

PRIOR FILING DATE: 2000-01-24

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 43008

SEQ ID NO 39876
APPLICANT: Blaney, Joseph E. Jr.
TITLE OF INVENTION: DEVELOPMENT OF MUTATIONS USEFUL FOR
TITLE OF INVENTION: DEVELOPMENT OF MUTATIONS USEFUL FOR
TITLE OF INVENTION: DEVELOPMENT OF DENGUE VIRUSES AND CHIMERIC DENGUE VIRUSES
FILE REFERENCE: NIH214.001C1
CURRENT APPLICATION NUMBER: US/10/719,547
CURRENT FILING DATE: 2003-11-21
PRIOR APPLICATION NUMBER: US 60/293049
PRIOR FILING DATE: 2001-05-22
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 3390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 3390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 37; DB 6; Length 339
Pred. No. 1.4e+03;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.1%; Score 36.5; DB 5; Length 3
47.8%; Pred. No. 1.4e+02;
tive 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 EEKTPL----TTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 EEATPLGDGTPTVTAAAPEVTYA 43
                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Dengue 3 virus strain H87
US-10-719-547-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3315 EDKTPVTTWEDVP 3327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 EEKTPLTTAAXAP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 47.8°
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-614-150A-39876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: CARGILL, Michele
APPLICANT: CARGILL, Michele
APPLICANT: BEGOVICH, Ann
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OP DETECTION AND USES THEREOF
FILE REFERENCE: CLO01490
CURRENT APPLICATION NUMBER: US/60/519,270
CURRENT FILING DATE: 2003-11-13
NUMBER OF SEQ ID NOS: 14048
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 229
LENGTH: 1064
                                                                                                                                                                                                                                                                                                                                                                                                     Expressed Nucleic Acid Sequences as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                               GENERAL INFORMATION:
APPLICANT: Mayo Foundation for Medical Education and Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.7%; Score 37; DB 6; Length 1064; ilarity 61.5%; Pred. No. 4.1e+02; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.7%; Score 37; DB 7; Length 1064;
61.5%; Pred. No. 4.1e+02;
tive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                   APPLICANT: Burgart, Lawrence
APPLICANT: Boardman, Lisa A.
APPLICANT: Thibodeau, Steven
APPLICANT: Lewis, Marcia
TITLE OF INVENTION: Use of Differentially E
TITLE OF INVENTION: Biomarkers for Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 1657/2022
CURRENT APPLICATION NUMBER: US/10/700,439
CURRENT FILING DATE: 2003-11-04
NUMBER OF SEQ ID NOS: 186
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 142
LENGTH: 1064
                                                                                                                                                                          Burgess, Christopher
Myerow, Susan
Thiagalingam, Arunthathi
Maimonis, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 229, Application US/60519270 GENERAL INFORMATION:
                                                                             Sequence 142, Application US/10700439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22, Application US/10719547; GENERAL INFORMATION: APPLICANT: Whitehead; APPLICANT: Mirphy, Brian R.
                                                                                                                                                  Bayer Healthcare LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1048 ESSTPGTTAASMP 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1048 ESSTPGTTAASMP 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 EEKTPLTTAAXAP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 EEKTPLTTAAXAP 14
                                                                                                                                                                                                                                                                            Molino, Gary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-700-439-142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-60-519-270-229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-60-519-270-229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 34
US-10-719-547-22
                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
```

qq

8

g

à

ö

```
RESULT 39
US-10-425-114A-52153
                                                                                                                                                                                                                                                                                                                                                                   US-10-739-930-9368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 52153
                                                                                                                                                                                                                                              LENGTH: 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CLOODY, NUMBER: US/09/614,150A
CURRENT APPLICATION NUMBER: US/09/614,150A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14309, Application US/10679063
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INTURNION:
TILLE OF INTURNION:
FILE REFERENCE: 38-15 (52054) B
CURRENT APPLICATION NUMBER: US/10/679,063
CURRENT PILING DATE: 2003-10-02
PRIOR PILING DATE: 2002-10-02
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 27373
SEQ ID NO 14309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.4%; Score 36; DB 5; Length 208; 57.1%; Pred. No. 1.1e+02; ive 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 6; Length 242;
Pred. No. 1.3e+02;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 864
LENGTH: 208
                                                                                                                                                                                                                                        CURRENT FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR PLILING DATE: 1999-10-05
PRIOR PLILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR PELING DATE: 1999-10-28
PRIOR FILING DATE: 1999-11-22
PRIOR FILING DATE: 1999-11-12
PRIOR PELING DATE: 1999-11-28
PRIOR PELING DATE: 1999-11-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR PELING DATE: 2000-01-12
                 Sequence 864, Application US/09614150A GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 PLAVAAPAPVLRTA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223 PITVAAAGPSVNN 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 PLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Vitis vinifera
US-10-679-063-14309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: DROSOPHILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-679-063-14309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-614-150A-864
US-09-614-150A-864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

RESULT 38

g

```
Sequence 9368, Application US/10739930
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
TITLE OF PAPPLICATION OF PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REPERENCE: 38-21(53377)B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT PILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEQ ID NOS: 11088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cao, Yongwein Title Or INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement PILE REPRENCE: 38-21(53313) B CURRENT APPLICATION NUMBER: US/10/425,114A CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

44.4%; Score 36; DB 6; Length 262
Best Local Similarity 72.7%; Pred. No. 1.4e+02; Aatches 8; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Clone ID: GLYMA-23APR03-C7814_17.p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: LIB3959-022-G10_FLI.pep
US-10-425-114A-52153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB 6; Le
Pred. No. 1.6e+02;
4; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 40
US-10-425-114A-51755
; Sequence 51755, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 52153, Application US/10425114A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhou, Yihua
Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 LTSSATAPVLSDA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 LTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 TPLTTAAXAPV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 TPSTAAAPAPV 49
                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
```

```
; CURRENT APPLICATION NUMBER: US/10/425,114A
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3067-037-E9_FLI.pep
US-10-425-114A-51755

Query Match
Best Local Similarity 53.8%; Pred. No. 1.76+02;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
OY 7 LTTAAXAPVXXNA 19
Db 132 LTSSATAPVLSDA 144

Search completed: January 28, 2004, 13:11:50
Job time: 23 secs
```

THIS PAGE BLANK (WARTON)

Thu Jan 29 11:56:40 2004

```
Arabidopsis thalia
Arabidopsis thalia
Escherichia coli p
Amino acid sequenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P. aeruginosa prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas aerugi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                           January 28, 2004, 13:02:13; Search time 41 Seconds (without alignments) 73.556 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
| SIDSI/gcgdata/geneseqp-embl/AA1984.DAT:*
| SIDSI/gcgdata/geneseqp-embl/AA1986.DAT:*
| SIDSI/gcgdata/geneseqp-embl/AA1987.DAT:*
| SIDSI/gcgdata/geneseqp-embl/AA1997.DAT:*
| SIDSI/gcgdata/geneseqp-embl/AA1997.DAT:*
| SIDSI/gcgdata/geneseqp-embl/AA1997.DAT:*
| SIDSI/gcgdata/geneseqp-embl/AA1997.DAT:*
| SIDSI/gcgdata/geneseqp-embl/AA1997.DAT:*
| SIDSI/gcgdata/geneseqgp-embl/AA1997.DAT:*
| SIDSI/gcgdata/geneseqgp-embl/AA1997.DAT:*
| SIDSI/gcgdata/geneseqgpeneseqp-embl/AA1997.DAT:*
| SIDSI/gcgdata/geneseqgpeneseqp-embl/AA1997.DAT:*
| SIDSI/gcgdata/geneseqggeneseqp-embl/AA1997.DAT:*
| SIDSI/gcgdata/geneseqggeneseqp-embl/AA1997.DAT:*
| SIDSI/gcgdata/geneseqggeneseqp-embl/AA1999.DAT:*
| SIDSI/gcgdata/geneseqggeneseqp-embl/AA2000.DAT:*
| SIDSI/gcgdata/geneseqggeneseqp-embl/AA2001.DAT:*
| SIDSI/gcgdata/geneseqggeneseqp-embl/AA2001.DAT:*
| SIDSI/gcgdata/geneseqggeneseqp-embl/AA2001.DAT:*
| SIDSI/gcgdata/geneseqggeneseqp-embl/AA2001.DAT:*
| SIDSI/gcgdata/geneseqggeneseqp-embl/AA2001.DAT:*
| SIDSI/gcgdata/geneseqggeneseqp-embl/AA2001.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                                                                                                                                      1107863
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                          1107863 segs, 158726573 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                      - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG30091
AAG30090
ABB52865
AAB67588
AAG30089
AAG43604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW64480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB69062
                                                                                                                                                                                                                                                               1 XEEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A_Geneseq_19Jun03;*
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                    US-09-359-426C-2
81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292
306
306
427
172
215
                    Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.3
54.3
54.3
51.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                    OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š.
```

| dopsis | ess | Drosophila melanog | eria mor | siell | -type | HIV isolate 5180 g | Benzodiazepines bi | Drosophila melanog | Drosophila melanog | . Drosophila melanog | | dia | - | ed Inte | amicum p | SPAS-1 | tumour | al | Drosophila melanog | щe | Human protein sequ | | Human lung cancer | C glutamicum prote | da alb | Novel human DNA-bi | Human DNA-binding | Phospholipase D to | $_{ m drog}$ | Streptomyces virid | Human LEKTI protei | Human circulating | hali | Arabidopsis thalia | erium l | |
|--------|-----|--------------------|----------|-------|----------|--------------------|--------------------|--------------------|--------------------|----------------------|------------|-----|----|----------|----------|------------|--------|----------|--------------------|----------|--------------------|----------|-------------------|--------------------|----------|--------------------|-------------------|--------------------|--------------|--------------------|--------------------|-------------------|----------|--------------------|----------|--|
| ~ | 315 | 592 | œ | 3610 | AAR51691 | 307 | 745 | 5058 | 5802 | 96 | 696 | 33 | 2 | ABG77349 | 0 | AAE22281 | 8 | AAE22283 | ABB67966 | ABB71511 | AAB94775 | ABB81876 | AAU81227 | AAG91455 | ABP73930 | AAU18229 | ABG92650 | AAR07361 | AAR63672 | 339 | 761 | 112 | AAG18092 | 0545 | ABP66095 | |
| 21 | 24 | 22 | 23 | 22 | 15 | 20 | 24 | 22 | 22 | 22 | 21 | 22 | 23 | 23 | 22 | 23 | 23 | 23 | 22 | 52 | 22 | 23 | 23 | 22 | 23 | 22 | 23 | 11 | 12 | 24 | 22 | 23 | 21 | 21 | 23 | |
| 3 | 13 | н | 2 | 445 | 6 | 9 | 0 | 8 | ~ | 79 | $^{\circ}$ | m | S | S | m | $^{\circ}$ | σ | σ | 4 | a | N | 229 | N | 9 | ~ | 7 | ~ | 0 | $^{\circ}$ | m | 19 | 87 | 120 | 4 | σ | |
| 51.9 | 。 | ٥. | δ. | 9. | 6 | 9 | 6. | σ | 9. | 8 | 8 | 8 | ъ. | 8 | 8 | 8 | 8 | • | 7. | 9 | 9 | 46.9 | 9 | • | ė. | ÷ | 9 | ė. | 9 | ė | 5 | ď. | ď. | 'n. | 5. | |
| | | | | 40 | | 40 | 40 | 40 | 40 | 39.5 | m | 39 | 39 | 39 | 39 | 39 | 39 | 39 | 38.5 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 37 | 37 | 37 | 37 | 37 | |
| 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 56 | 27 | 28 | 53 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | 1 | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

ALIGNMENTS

RESULT 1

P. aeruginosa protein antigen Pa60 N-terminal peptide fragment Antigen; Pa60; diagnosis; detection; cystic fibrosis; vaccine; Location/Qualifiers AAW64480 standard; peptide; 19 AA. immunogen; infection; treatment /label= unknown /label= unknown /label= unknown 98WO-GB00217. 97GB-0001489 20-OCT-1998 (first entry) Pseudomonas aeruginosa Misc-difference 13 Key Misc-difference Misc-difference 26-JAN-1998; 24-JAN-1997; WO9832769-A1 30-JUL-1998 AAW64480; AAW64480

(AUSP-) AUSPHARM INT LTD.

ö

Gaps

4X1X4X47475X8X000000X8

ઠે

```
The present invention describes antigenic Pseudomonas aeruginosa proteins (P1). The P. aeruginosa proteins have antibacterial activity and can be used in vaccines and as antagonists. The proteins or their fragments, or antibodies are useful in the detection and/or diagnosis of P. aeruginosa. They are also useful for producing a vaccine and inducing an immune response against P. aeruginosa infection. An agent capable of antagonising, inhibiting or otherwise interfering with the function or expression of P1 are useful in the manufacture of a medicament for the treatment or prophylaxis of P. aeruginosa infections. The present sequence represents a probable P. aeruginosa infections. N-terminal peptide sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                          93.8%; Score 76; DB 22; Length 19; 100.0%; Pred. No. 3.6e-06; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana protein fragment SEQ ID NO: 35912.
                                                                                                                                                                                                                                                                                                                                                                       AAG30091 standard; Protein; 291 AA.
                                                                                                                                                                                                                                                                     2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                               2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0128234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0123548
99US-0125788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0126264
99US-0126785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0130510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0131449
99US-0132048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0132407
99US-0132484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0134370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-FEB-2000; 2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0129845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0130449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0130891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0132485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0132486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0132487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0132863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0134256
                                                                                                                                                                                                                                                                                                                                                                                                                              17-OCT-2000 (first entry)
                                                                                                                                                                                                                                        18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     termination sequence
                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                   19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAY-1999;
14-MAY-1999;
18-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-1999;
29-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                   AAG30091;
                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                              RESULT 3
                                                                                                                                                                                                                                                                                                                                                          AAG30091
           g
                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                This peptide is the N-terminal fragment of a novel Pseudomonas aeruginosa protein antigen, Pa60. This fragment could be used for diagnostic detection of P. aeruginosa by forming complexes with specific antibodies, particularly in patients with cystic fibrosis (by analysis of mucus, e.g. in saliva), or in vaccines or immunogenic compositions to treat or prevent infection by P. aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antigenic Pseudomonas aeruginosa proteins, useful in the detection and/or diagnosis of P. aeruginosa infections and for producing vaccines against P. aeruginosa -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sizer PJH, Wilkinson MC;
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa; chitinase; groEL; chiA; antigen; vaccine; diagnosis; detection; infection; immune response.
                                                                                               Protein antigen from Pseudomonas aeruginosa and its antigenic fragments - useful diagnostically to detect specific antibodies, particularly in patients with cystic fibrosis, and as vaccines
                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                 Length 19;
                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas aeruginosa protein N-terminal peptide.
                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                 DB 19; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peek K,
                                                                                                                                                                                                                                                                                                                93.8%; Score 76; DB 100.0%; Pred. No. 3.6
                                         Kyd J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "unspecified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "unspecified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "unspecified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith MW,
                                         Dunkley M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 2; 129pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB69062 standard; peptide; 19 AA.
                                                                                                                                                                                                                                                                                                                                                                          EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                     EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                        Claim 3; Page 2; 23pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-JUL-2000; 2000WO-GB02554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99GB-0015419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 100...
Local 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith CJ, Thompson SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PROV-) PROVALIS UK LTD
                                         Clancy RL, Cripps AW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa
             (CHAP/) CHAPMAN P W.
                                                                    WPI; 1998-427879/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-080988/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 12
                                                                                                                                                                                                                                                                                      19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200102577-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                            ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB69062;
                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB69062
```

| - SU6 - SU6 | 99US-014741 99US-014749 99US-014817 99US-014814 99US-014886 99US-014886 99US-014986 99US-014972 99US-014972 99US-014992 | - Sn66 - | 9905-015/86 9905-015/80 9905-015/80 9905-015/80 9905-015/90 9905-015/90 9905-015/90 9905-016/07/99 9905-016/07/99 9905-016/07/99 |
|---|--|---|--|
| AUG-1 | 6-AUG-1 9-AUG-1 0-AUG-1 11-AUG-1 2-AUG-1 3-AUG-1 0-AUG-1 0-AUG-1 0-AUG-1 3-AUG-1 3-AUG-1 3-AUG-1 5-AUG-1 | AUG-1 | 06-0CT-1999; 07-0CT-1999; 13-0CT-1999; 13-0CT-1999; 14-0CT-1999; 14-0CT-1999; 14-0CT-1999; 14-0CT-1999; 14-0CT-1999; 12-0CT-1999; 21-0CT-1999; 22-0CT-1999; 22-0CT-1999; 25-0CT-1999; 25-0CT-1999; 26-0CT-1999; |
| | X X X X X X X X X X X X X X X X X X X | *************************************** | |
| | | | |
| | | | • |
| | | | |
| · | | ` | |
| 941. 1124. 629. 629. 7392. 7392. 528. 500. | C O O O O U L 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | 4 6 7 8 9 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 | 44444444444444444444444444444444444444 |
| 90S-013 90S-013 90S-013 90S-013 90S-013 90S-013 90S-013 | 905-013 906-013 906-013 906-013 906-013 906-013 906-013 906-013 906-013 906-013 906-013 | 905-013 | |
| MAY-1 MAY-1 MAY-1 MAY-1 MAY-1 MAY-1 UUN-1 | | | 16-001-1999; 16-001-1999; 16-001-1999; 19-001-1999; 19-001-1999; 19-001-1999; 19-001-1999; 20-001-1999; 21-001-1999; 21-001-1999; 22-001-1999; 22-001-1999; 23-001-1999; 23-001-1999; 23-001-1999; 23-001-1999; 23-001-1999; 23-001-1999; 24-001-1999; 25-001-1999; 27-001-1999; 27-001-1999; 27-001-1999; 27-001-1999; |
| PR P | X X X X X X X X X X X X X X X X X X X | % % % % % % % % % % % % % % % % % % % | \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ |

```
99US-0137724.
99US-0138094.
99US-0138540.
99US-0138847.
                                                                                                                                                                                                                                                                                                                                                 99US-0145086.
99US-0145088.
99US-0145085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0147038.
99US-0147204.
99US-0147302.
                                                                                                                                                                                                                                                                                                                       99US-0144352.
                                           99US-0139119
99US-0139452
                                                                                                                                                 99US-0139817
99US-0139899
                                                                                                                                                                                               99US-0141287
99US-0141842
                                                                                                                                                                                                                                                                                                                                                                    99US-0145087
                                                                                                                                                                                                                                                                                                                                                                                 99US-0145192
99US-0145145
                                                                                                                                                                                                                                                                                                                                                                                              99US-0145218
99US-0145224
                                                                                   99US-0139456
                                                                                                                                                                                                                 99US-0142055
99US-0142390
                                                                                                                                                                                                                                      99US-0142920
                                                                                                                                                                                                                                           99US-0142977
99US-0143542
                                                                                                                                                                                                                                                                                  99US-0144325
                                                                                                                                                                                                                                                                                        99US-0144331
99US-0144332
                                                                                                                                                                                                                                                                                                                                     99US-0144884
99US-0144814
                                                                                                                                                                                                                                                                                                                                                                                                           99US-0145276
99US-0145913
                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0145918
                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0145919
99US-0145951
                                                                                                                                                                                                                                                                                                                  99US-0144335
                                                                                                                   99US-0139461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-AUG-1999;
04-AUG-1999;
                                                                                                                                                                                                            1-JUL-1999
                                                                                                                                                                                                                                                                                                     9-JUL-1999
ö
                                                                                                                                                                     Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                          Gaps
                                                          .
0
                                           Score 44; DB 21; Length 291;
Pred. No. 21;
2; Mismatches 4; Indels
                                                                                                                                                         Arabidopsis thaliana protein fragment SEQ ID NO: 35911.
                                                                                                                   AAG30090 standard; Protein; 292 AA.
     990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
                                                                                                                                                                                                                                                 99US-0121825.
99US-0123180.
99US-0123548.
99US-0125788.
                                                                                                                                                                                                                                                                                                           990S-0129845.
990S-0130077.
990S-0130510.
990S-0130891.
990S-0131449.
                                                                                                                                                                                                                                                                                                                                                        990S-0132407.
990S-0132484.
990S-0132485.
990S-0132486.
990S-0132487.
990S-0134287.
                                                                                                                                                                                                                                                                                         99US-0127462.
99US-0128234.
99US-0128714.
                                            Query Match 54.3%;
Best Local Similarity 60.0%;
Matches 9; Conservative
99US-0161360
                                                                      EEKTPLTTAAXAPVV 16
                                                                              ||| :||| :|||
EEKAEMTTAMOSPVV 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0136392
99US-0136782
                                                                                                                                                                                                                                      25-FEB-2000; 2000EP-0301439
                                                                                                                                                                                                                                                                                   99US-0126785
                                                                                                                                             17-OCT-2000 (first entry)
                                                                                                                                                                                               Arabidopsis thaliana
     26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
29-0CT-1999;
                                                                                                                                                                                                            EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-MAY-1999;
28-MAY-1999;
                                                                                                                                                                                                                         06-SEP-2000
                                                                                                                                AAG30090;
                                                                                   72
                                                                                                                                                                                                                                                                                                                                -APR-
                                                                                                       RESULT 4
R R R R R R
                                                                       ò
                                                                                   원
```

```
99US-0151065.
99US-0151066.
99US-0151080.
99US-0147192.
99US-0147303.
99US-0147416.
99US-0147416.
99US-0147935.
99US-0148171.
99US-0148171.
99US-0148171.
99US-0148171.
99US-0148542.
99US-0149175.
99US-0149175.
99US-0149175.
99US-0149929.
99US-0149930.
99US-0149930.
                                                                                                                                                                                                                                                                       99US-0151303.
99US-0151438.
99US-0151930.
99US-0152363.
                                                                                                                                                                                                                                                                                                                                                                                                99US-0155659
99US-0156458
99US-0156458
99US-0157117
99US-0157865
99US-0158029
99US-0158029
99US-0158232
99US-015929
99US-015929
99US-015929
99US-0159330
99US-0159330
99US-0159330
99US-0159330
99US-0159331
99US-0159331
99US-0159331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               990S-0161361
990S-0161920.
990S-0161992.
990S-0161993.
                                                                                                                                                                                                                                                                                                                     99US-0153070
                                                                                                                                                                                                                                                                                                                                 99US-0153758
99US-0154018
                                                                                                                                                                                                                                                                                                                                                                           99US-0155139
99US-0155486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0160815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0160981
                                                                                                                                                                                                                                                                                                                                                      99US-0154039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0160814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0161404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0161405
                                           09-AUG-1999;
09-AUG-1999;
10-AUG-1999;
11-AUG-1999;
12-AUG-1999;
13-AUG-1999;
                                                                                                                                                                                           23-AUG-1999;
23-AUG-1999;
25-AUG-1999;
                                                                                                                                                                     20-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                                        27-AUG-1999
                                                                                                                                                                                                                                                  27-AUG-1999
27-AUG-1999
                                                                                                                                                                                                                                                                         30-AUG-1999
                                                                                                                                                                                                                                                                                    31-AUG-1
```

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a library of DNA fragments of Escherichia colistrains comprising polynucleotides (ABA88577-ABA88729 and ABA89533) and and encoded proteins (ABB52459-ABB52919 and ABB52954-ABB53094) of nature BZ/D+A. The polynucleotides have potential antiinflammatory, antibacterial and immunosuppressive activity as part of pharmaceutical compositions used to treat, palliate or prevent extra-intestinal E. coliinfections. The polypeptides are useful for determining the phylogenic group of a given. E. coli strain. These polypeptides can detect and treat an undesired development of E. coli, particularly an extra-intestinal infection that include systemic and non-diarrhoeal infections such as septicaemia, pyelonephritis and meningitis this is particularly advantageous as bacterial resistance is increasing with the more frequent use of broad spectrum antibiotics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A library of DNA fragments of Escherichia coli strains for the phylogenic determination of a given strain comprises polynucleotides of nature B2/D+A-
                                                                                                                                                                                                                                                                                                                         Escherichia coli; B2/D+A-; antiinflammatory; antibacterial; immunosuppressive; extra-intestinal infection; phylogeny; meningitis; systemic infection; non-diarrhoeal infection; septicaemia; phylosphritis; antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.3%; Score 44; DB 22; Length 306; 47.1%; Pred. No. 22; 6; Indels tive 3; Mismatches 6; Indels
54.3%; Score 44; DB 21; Length 292; 60.0%; Pred. No. 21; ive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clermont O, Nassif X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                          Escherichia coli polypeptide SEQ ID NO 1139.
                                                                                                                                                                                         ABB52865 standard; Protein; 306 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 6; Fig 6; 646pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | | | :: | |: | | EKVPCTSSGVAPIFVNA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-2001; 2001WO-EP03445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAR-2000; 2000FR-0003145.
02-FEB-2001; 2001FR-0001449.
                                                                    2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                          11-FEB-2002 (first entry)
                                                                                         ||| :||| EEKAEMTTAMQSPVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 47.1
nes 8; Conservative
                                     9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bonacorsi S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-550253/61.
              Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306 AA;
                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200166572-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bingen E,
                                                                                                                                                                                                                        ABB52865;
                                                                                                    73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loca
Matches
                                                                                                                                                                       ABB52865
                                                                                                                                                         RESULT
                                                                      8
                                                                                                    엄
                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
```

RESULT

```
hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                         99US-0135
                                                                                                                                                                                                                                                                                                                                                                                     99US-01
                              Arabidopsis thaliana
            termination sequence
                                                                                          25-FEB-2000;
                                                   EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUN-1999
                                                                                                                                                                                                                                                                                                        06-MAY-1999
                                                                                                                                                                                                                                                                                                                                               4-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                   4-MAY-1999,
                                                                                                                                                                                                               9-APR-1999
                                                                      06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                 .9-MAY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-MAY-
                                                                                                                                                                                                                                                                                                                                                                                                                             24 - MAY -
 ö
                                                                                                                                                                                                                                                                                                                                               In vitro enzymatic synthesis of deoxyribonucleosides comprises reacting deoxyribose 1-phosphate and a nucleobase to form a deoxyribonucleoside and an inorganic phosphate -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enzymes which
                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a deoxyribokinase enzyme. This enzyme is involved in the biosynthesis of deoxyribonucleosides, and is used in the method of the invention. The specification describes a method for the in vitro enzymatic synthesis of deoxyribonucleosides. The method comprises reacting deoxyribose 1-phosphate and a nucleobase to form a deoxyribonucleoside and an inorganic phosphate. Bnzymes which may be used in the method of the invention include thymidine phosphorylase, purine nucleoside phosphorylase, phosphopentose aldolase, fructose 1,6-diphosphate aldolase, and nucleoside 2-deoxyriboshtransferase.
                                                                                            Deoxyribonucleoside; deoxyribose 1-phosphate; thymidine phosphorylase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                     Ihlenfeldt H, Barzu O, Sakamoto H, Pistotnik E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.3%; Score 44; DB 22; Length 306;
llarity 47.1%; Pred. No. 22;
Conservative 3; Mismatches 6; Indels
                                                                                                      purine nucleoside phosphorylase; phosphopentose mutase; phosphopentose aldolase; fructose 1,6-diphosphate aldolase; deoxyribokinase; nucleoside 2-deoxyribosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana protein fragment SEQ ID NO: 35910.
                                                                          Amino acid sequence of a deoxyribokinase enzyme
                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 59-61; 73pp; English.
                                                                                                                                                                                                                                                                 (PHAR-) PHARMA-WALDHOF GMBH & CO KG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ä.
              AAB67588 standard; Protein; 306 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG30089 standard; Protein; 427
                                                                                                                                                                                                                                              (HOFF ) ROCHE DIAGNOSTICS GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 EKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                         18-AUG-2000; 2000WO-EP08088.
                                                                                                                                                                                                                           99EP-0116425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                 Marliere P, Pochet S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-235026/24.
                                                                                                                                                                                                                                                                                                                               N-PSDB; AAF55444.
                                                                                                                                               Salmonella typhi.
                                                                                                                                                                  WO200114566-A2
                                                                                                                                                                                                                             20-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-0CT-2000
                                                      29-MAY-2001
                                                                                                                                                                                      01-MAR-2001
                                                                                                                                                                                                                                                                                       Tischer W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG30089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                  AAB67588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG30089
       AAB67588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
```

```
99US-0139458.
99US-0139459.
99US-0139460.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0138540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0139456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0139750
                                                99US-0128234.
                                                                                                                                                                                                                          99US-0132863
                                                                                                                                                                                                                                        99US-0134256.
                                                                                                                                                                                                                                                  99US-0134218.
                                                                                                                                                                                                                                                                                        99US-0134370
                                                                                                                                                                                                                                                                                                                                                                          99US-0136392
99US-0136782
                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0137724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0139492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0139461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0139899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0140354
99US-0125788
99US-0126264
                        99US-0126785
                                     99US-0127462
                                                                          99US-0129845
                                                                                                  99US-0130449
                                                                                                                                     99US-0131449
                                                                                                                                                  99US-0132048
                                                                                                                                                                          99US-0132484
                                                                                                                                                                                       99US-0132485
                                                                                                                                                                                                  99US-0132486
                                                                                                                                                                                                               99US-0132487
                                                                                                                                                                                                                                                                           99US-0134221
                                                                                                                                                                                                                                                                                                               99US-0134941
                                                                                                                                                                                                                                                                                                                                                    99US-0135629
                                                                                                                                                                                                                                                                                                                                                                                                                99US-0137528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0139119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0139452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0139453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0139455
                                                                                    99US-0130077
                                                                                                                          99US-0130891
                                                                                                                                                              99US-0132407
```

```
990S - 0140695 - 990S - 0140695 - 990S - 0140823 - 990S - 0141287 - 990S - 0141287 - 990S - 0142055 - 990S - 0142055 - 990S - 014205 - 990S - 014205 - 990S - 014205 - 990S - 014205 - 990S - 0144325 - 990S - 0144334 - 990S - 0144325 - 990S - 014508 - 990S - 014708 - 014708 - 990S - 014708 - 990S - 014708 - 990S - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 - 014708 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    990S-0148319
99US-0148319
99US-0148341
99US-0148684
99US-0149368
99US-0149426
99US-0149426
99US-0149722
99US-0149929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0149930.
99US-0150566.
99US-0150884.
99US-0151065.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0151066.
99US-0151080.
99US-0151303.
99US-0151438.
99US-0151930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-AUG-1999;
20-AUG-1999;
20-AUG-1999;
23-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3-AUG-1999
```

```
Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                           Score 44; DB 21; Length 427;
Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana protein fragment SEQ ID NO: 54519.
                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG43604 standard; Protein; 172 AA
                                                                                                                                                                                                                                                                                                                                                                                            5,
      990S-0153070.
990S-0153758.
990S-0154018.
990S-0154039.
                                                                                                                                                                                                                                                                                                                                                                             54.3%;
                                              99US-0155139.
99US-0155486.
99US-0155659.
99US-0156458.
                                                                                                                                                                                                                                                                                                                                                                                                                     ||| :||| :|||
208 EEKAEMTTAMQSPVV 222
                                                                               99US-0156596
99US-0157117
                                                                                               99US-0157753
99US-0157865
                                                                                                                99US-0158029
                                                                                                                       99US-0158232
99US-0158369
                                                                                                                                      99US-0159293
99US-0159294
                                                                                                                                                       99US-0159295
                                                                                                                                                              99US-0159329
                                                                                                                                                                       99US-0159330
                                                                                                                                                                               99US-0159331
99US-0159637
                                                                                                                                                                                              99US-0159638
                                                                                                                                                                                                       99US-0159584
                                                                                                                                                                                                                               99US-0160768
                                                                                                                                                                                                                                              99US-0160814
                                                                                                                                                                                                                                                      99US-0160815
                                                                                                                                                                                                                                                              99US-0160980
99US-0160981
                                                                                                                                                                                                                                                                                                     99US-0161406
99US-0161359
                                                                                                                                                                                                                                                                                                                     99US-0161360
99US-0161361
                                                                                                                                                                                                                                                                                                                                                              99US-0162142
                                                                                                                                                                                                                                                                                                                                                                                                            2 EEKTPLITAAXAPVV 16
                                                                                                                                                                                                                99US-0160741
                                                                                                                                                                                                                      99US-0160767
                                                                                                                                                                                                                                                                                       99US-0161404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                             9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
07-SEP-1999;
10-SEP-1999;
13-SEP-1999;
15-SEP-1999;
16-SEP-1999;
22-SEP-1999;
23-SEP-1999;
                                                               24-SEP-1999
                                                                               29-SEP-1999;
04-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                             29-OCT-1999;
                                                                                                                                                                                                                                                                                                              26-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG43604;
                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                          셤
```

EP1033405-A2

```
990S - 0.142977
990S - 0.143542
990S - 0.144062
990S - 0.144085
990S - 0.144086
990S - 0.144331
990S - 0.144331
990S - 0.144332
990S - 0.144333
                                                                                                                                                                                                                                                                   990S-0147493
990S-0148171
990S-0148131
990S-0148131
990S-0148545
990S-0148684
990S-0148684
990S-0149175
990S-0149172
990S-0149723
990S-0149723
990S-0149930
990S-0149930
990S-0149930
990S-0149930
990S-0150656
990S-0150656
                                                                                                                                                                                                                                                                                                                                                                                     990S-0151080
990S-0151303
990S-0151303
990S-0151930
990S-0152363
990S-0153758
990S-0153758
990S-0154018
990S-0154739
                                                                                          99US-0144352.
99US-0144632.
99US-0144884.
99US-0144814.
99US-0145086.
                                                                                                                                                      99US-0145145.
99US-0145218.
99US-0145224.
                                                                                                                                                                                                99US-0145951.
99US-0146386.
99US-0146388.
                                                                                                                                                                                                                                           99US-0147192.
99US-0147260.
99US-0147303.
99US-0147416.
99US-0142390
      99US-0142803
99US-0142920
                                                                                                                              99US-0145085
                                                                                                                                          99US-0145089
                                                                                                                                                                         99US-0145276
                                                                                                                                                                                     99US-0145918
99US-0145919
                                                                                    99US-0144335
                                                                                                                                                                                                                          99US-0147038
                                                                                                                                                                                                                               99US-0147204
99US-0147302
                                                                                                                                      99US-0145087
                                                                                                                                                                                99US-0145913
                                                                                                                                                                                                                   99US-0146389
                                                                                                                                                                                                                                                                                                              16-AUG-1999;
17-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                   23-AUG-1999
23-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                     26-AUG-1999
27-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                 27-AUG-1999
27-AUG-1999
                                                                                                                                                                                                                                                                                                                                       20-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                25-AUG-1999
990S-0138540
990S-0138847
990S-0139119
990S-0139453
990S-0139454
990S-0139454
990S-0139456
990S-0139456
                                                                                                                         99US-0132407-
99US-0132484-
99US-0132486-
99US-0132487-
99US-0132487-
99US-0134218-
99US-0134218-
99US-0134219-
99US-0134219-
99US-0134219-
99US-0134219-
99US-0134370-
99US-0134370-
99US-013533-
99US-013532-
99US-0135621-
99US-0135621-
99US-0135621-
99US-0135621-
99US-0135621-
99US-0135621-
                                                                                                                                                                                                                                                                                                                                              99US-0139459.
99US-0139460.
99US-0139461.
99US-0139462.
                        99US-0121825.
99US-0123548.
99US-0123548.
99US-0125788.
99US-0126785.
99US-0126785.
99US-0128714.
99US-012814.
99US-012814.
99US-012814.
99US-0130449.
99US-013049.
                                                                                                                                                                                                                                                                                                                                                                      99US-0139463.
99US-0139750.
99US-0139763.
                                                                                                                                                                                                                                                        99US-0137502.
99US-0137724.
99US-0138094.
                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0141287
99US-0141842
99US-0142154
99US-0142055
             25-FEB-2000; 2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1999
02-JUL-1999
 06-SEP-2000
```

```
990S-0127462.
990S-0128234.
990S-0128714.
990S-0130877.
990S-0130449.
                                                                                                                                                                                                    99US-0134218.
99US-0134219.
99US-0134221.
99US-0134370.
                                                                                                                                                                                                                                                                                                                                                         99US-0137724.
99US-0138540.
99US-0138547.
99US-0139119.
99US-0139452.
                                                                                                   99US-0130891.
99US-0131449.
99US-0132048.
                                                                                                                                99US-0132407.
99US-0132484.
99US-0132485.
99US-0132486.
                                                                                                                                                                        99US-0132863.
99US-0132863.
99US-0134256.
                                                                                                                                                                                                                                             99US-0134768.
99US-0134941.
99US-0135124.
99US-0135353.
                                                                                                                                                                                                                                                                                   99US-0135629.
99US-0136021.
99US-0136392.
                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0139454.
99US-0139454.
99US-0139455.
99US-0139456.
99US-0139457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0139460.
99US-0139461.
99US-0139462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0139750.
99US-0139763.
99US-0139817.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0139899.
99US-0140353.
99US-0140354.
99US-0140695.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0142920.
99US-0142920.
99US-0142977.
99US-0143542.
99US-0143624.
                                                                                                                                                                                                                                                                                                                 99US-0136782.
99US-0137222.
99US-0137528.
99US-0137502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0140823.
99US-0140991.
99US-0141287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0142154.
99US-0142055.
99US-0142390.
             99US-0126264
99US-0126785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0139463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .8-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUN-1999
29-JUN-1999
                                                                                                                                                                                                                                                                                                                                                  04-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                      6-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                 7-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                         8-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 - JUN - 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JUN-1999
                                                                                                                                                                                                                                                                                                                              -JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                  DB 21; Length 172;
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 54518.
                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                           ed. No. 25;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 Score 42;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG43603 standard; Protein; 215 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 EEKTPVEKKTGVPVVKKA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                        EEKTPLTTAAXAPVVXNA 19
990S-0155486

990S-0156458

990S-0156559

990S-0156565

990S-0156565

990S-0157753

990S-0157753

990S-0159293

990S-0159294

990S-0159294

990S-0159329

990S-0159330

990S-0159330

990S-0159330

990S-0159330

990S-0159330

990S-0159638

990S-0160767

990S-0160980

990S-0161960

990S-0161960

990S-0161960

990S-0161960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0121825.
99US-0123180.
99US-0123548.
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 50.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-FEB-2000; 2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                  28-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                         ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG43603;
                                                                                                                                                                                                                                                      22-OCT-1
22-OCT-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG43603
                                                                                                                                                                                                                                                                                                                                                                                                                                                           엄
                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠ
```

99US-0158029

```
990S-0148565
990S-0148684
990S-0149175
990S-0149175
990S-0149725
990S-0149723
990S-0149929
990S-0149902
990S-0149902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0150884.
99US-0151065.
99US-0151066.
99US-0151080.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0151303.
99US-0151438.
99US-0151930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         990S-0152363.
990S-0153070.
990S-0153078.
990S-0154018.
990S-0154039.
990S-0155139.
99US-0144086.
99US-0144086.
99US-0144325.
99US-0144332.
99US-0144333.
99US-0144333.
99US-0144335.
99US-0144335.
99US-0144335.
99US-0144632.
99US-0144632.
99US-0145086.
99US-0145086.
99US-0145086.
99US-0145086.
99US-0145085.
99US-0145089.
99US-0145319.
99US-0145319.
99US-0145319.
99US-0145318.
                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0148171.
99US-0148319.
99US-0148341.
                                                                                                                                                                                                                                                                                                                                                                04-AUG-1999;
05-AUG-1999;
05-AUG-1999;
06-AUG-1999;
                                                                                                                                                                                                                                                                                             28-JUL-1999;
02-AUG-1999;
02-AUG-1999;
02-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8-AUG-1999
                                                                                                                                                                                                                                                                                                                                         03-AUG-19
```

```
Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                Ouery Match 51.9%; Score 42; DB 21; Length 215; Best Local Similarity 50.0%; Pred. No. 32; Matches 9; Conservative 1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana protein fragment SEQ ID NO: 54517.
                                                                                                                                                                                                                                                                                                                                                                                  AAG43602 standard; Protein; 332 AA
                                                                                                                                                                                                                                                                                                                                |||||:
174 EEKTPVEKKTGVPVVKKA 191
                                                                                                                                                                                                                                                                                                                     2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0121825.
99US-0123548
99US-0123548
99US-0125788.
99US-0126785.
99US-0127462.
99US-0128134.
99US-0128114.
      990S - 0158232
990S - 0159293
990S - 0159293
990S - 0159295
990S - 0159325
990S - 0159330
990S - 0159331
990S - 0159638
990S - 0159638
990S - 0159638
990S - 0160741
990S - 0160741
990S - 0160980
990S - 0160980
990S - 0160980
990S - 0161406
990S - 0161406
990S - 0161406
990S - 0161406
990S - 01611406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-FEB-2000; 2000EP-0301439
                                                                                                                                                                                                                                                                99US-0162142
                                                                                                                                                                                                                                                                                                                                                                                                                   18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAR-1999;
01-APR-1999;
06-APR-1999;
08-APR-1999;
16-APR-1999;
                       13.0CT-1999
13.0CT-1999
14.0CT-1999
14.0CT-1999
14.0CT-1999
14.0CT-1999
14.0CT-1999
12.0CT-1999
21.0CT-1999
22.0CT-1999
22.0CT-1999
22.0CT-1999
22.0CT-1999
22.0CT-1999
22.0CT-1999
22.0CT-1999
22.0CT-1999
22.0CT-1999
23.0CT-1999
24.0CT-1999
25.0CT-1999
26.0CT-1999
26.0CT-1999
26.0CT-1999
26.0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                    AAG43602;
                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                     g
```

| 990S-0144335. 990S-0144352. 990S-0144884. 990S-0144814. 990S-0145086. 990S-0145088. 990S-0145087. | -0145 -0145 -0145 -0146 -0146 -0146 -0146 -0146 -0147 -0146 | 990S-0147260 990S-0147303 990S-0147405 990S-0147493 990S-0148171 990S-0148171 990S-0148341 990S-0148684 990S-0149368 990S-014975 990S-014975 990S-0149726 | 990S-0149929. 990S-0149930. 990S-0149930. 990S-015084. 990S-0151065. 990S-0151080. 990S-0151080. 990S-015138. 990S-015138. 990S-015138. | 990S-0155139 990S-0155486 990S-0156559 990S-0156596 990S-01571753 990S-0157853 990S-0158369 990S-0158369 990S-0158369 990S-0158369 990S-0158369 |
|--|--|--|--|---|
| | | | 20-AUG-1999; 23-AUG-1999; 23-AUG-1999; 25-AUG-1999; 27-AUG-1999; 27-AUG-1999; 30-AUG-1999; 31-AUG-1999; 01-SEP-1999; 01-SEP-1999; 11-SEP-1999; 11-SEP-1999; 11-SEP-1999; 11-SEP-1999; 11-SEP-1999; | 22-SEP-1999; 24-SEP-1999; 24-SEP-1999; 24-SEP-1999; 04-0CT-1999; 06-0CT-1999; 06-0CT-1999; 13-0CT-1999; 13-0CT-1999; 13-0CT-1999; 13-0CT-1999; |
| # # # # # # # # # # # # # # # # # # # | # # # # # # # # # # # # # # # # # # # | % | % | |
| | | | | |
| | | | | |
| | | | | |
| · | | | | |
| | | | | |
| | | | | |
| | | | | |
| | S0132487. S0134286. S0134218. S0134219. S0134221. S0134370. S0134370. S0135124. S0135124. S0135124. S0135124. S0135124. S0135124. S0135124. S0135123. | S-0137528 S-0137528 S-0137528 S-0137524 S-0138094 S-0138452 S-0139453 S-0139455 S-01 | 9US-0139459 9US-0139460 9US-0139461 9US-0139462 9US-0139463 9US-0139750 9US-0139750 9US-0139750 9US-0140353 9US-0140353 9US-0140695 9US-0140823 9US-0140823 9US-0140823 9US-0141287 9US-0141287 9US-0141287 | 0142055. 0142803 0142803 0142803 0142920 0143542 0144085 0144086 0144331 0144333 |
| 000000000000000000000000000000000000000 | 555555555555555555555555555555555555555 | | - SUBS S S S S S S S S S S S S S S S S S | |
| 9-APR-1999 1-APR-1999 3-APR-1999 3-APR-1999 3-APR-1999 1-APR-1999 1-APR-1999 1-MAY-1999 5-MAY-1999 | - MAY-1999 - MAY-1999 | 3. JUN -1999 4. JUN -1999 5. JUN -1999 8. JUN -1999 9. JUN -1999 9. JUN -1999 9. JUN -1999 9. JUN -1999 8. JUN -1999 8. JUN -1999 8. JUN -1999 | 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 22-JUN-1999; 22-JUN-1999; 23-JUN-1999; 23-JUN-1999; 23-JUN-1999; 23-JUN-1999; 24-JUN-1999; 24-JUN-1999; 30-JUN-1999; 30-JUN-1999; | 2. vul. 1999 9. vul. 1999 9. vul. 1999 9. vul. 1999 8. vul. 1999 8. vul. 1999 9. vul. 1999 9. vul. 1999 9. vul. 1999 |

```
23-MAR-2000; 2000US-191637P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 50.v.
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster.
                             Famodu 00,
                                   Sakai H,
                                                 WPI; 2003-198391/19.
N-PSDB; ABX78329.
                                                                                                                                                                                                                                                                                         132 AA;
(THOR/) THORPE C
      (SAKA/) SAKAI H.
(WENG/) WENG Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-SEP-2001
                                   Thorpe CJ,
                             Falco SC,
                                                                                                                                                                                                                                                                                                                                                                                                  ABB66926;
                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
                                                                                                                                                                                                                                                                                                                                                                              ABB66926
                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                               ö
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                    Plant; EST; expressed sequence tag; stress response; drought; heat; radiation; pathogen attack; grain flavour; disease resistance; peptide-methionine sulphoxide reductase; DNA repair; enzyme; intracellular protein transport.
                                                                                                                                                                                               .;
0
                                                                                                                                                                                DB 21; Length 332;
                                                                                                                                                                                               Indels
                                                                                                                                                                                               ..
8
                                                                                                                                                                                       ed. No. 52;
Mismatches
                                                                                                                                                                              51.9%; Score 42;
llarity 50.0%; Pred. No. !
Conservative 1; Mismatrd
                                                                                                                                                                                                                                                               ABU58158 standard; Protein; 132 AA.
                                                                                                                                                                                                                                                                                                        Rice stress response protein #4.
                                                                                                                                                                                                                           291 EEKTPVEKKTGVPVVKKA 308
                                                                                                                                                                                                              2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                       990S-133042P.
990S-133427P.
990S-133428P.
990S-133436P.
                      990S-0159638.
990S-0159584.
990S-0160741.
99US-0160767.
                                                                       99US-0160815.
99US-0160980.
99US-0160981.
                                                                                                                                            99US-0161920.
99US-0161992.
99US-0161993.
99US-0162142.
                                                                                                                                                                                                                                                                                                                                                                                                                 99US-133038P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-133438P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-137667P
                                                                                                                         99US-0161359
99US-0161360
                                                                                                                                                                                                                                                                                                                                                                                                   19-FEB-2002; 2002US-0078929
                                                         99US-0160770
99US-0160814
                                                                                            99US-0160989
                                                                                                     99US-0161404
                                                                                                           99US-0161405
                                                                                                                   99US-0161406
                                                                                                                                       99US-0161361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0566394
                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FALCO S C.
FAMODU O O.
MEYERS B C.
MIAO G.
ODELL J T.
RAFALSKI J A.
                                                                                                                                                                                        Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                       US2002152497-A1.
                                                                                                                                                                                                                                                                                                                                                          Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-MAY-2000;
                                                                                                                                                                                                                                                                                           14-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                      17-0CT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                         07-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                11-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                       11-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                               11-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-JUN-1999
                                                                                                                                                                                                                                                                             ABU58158;
                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MIAO/)
(ODEL/)
(RAFA/)
                                                                        21-OCT-1
                                                                                -OCT-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FALC/)
                                                                                                           25-OCT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FAMO/)
(MEYE/)
                                                                                                                                                                                                                                                RESULT 11
                                                                                                                                                                                                                                                       ABUS8158
ID ABUS
                                                                                                                                                                                                                                                                     g
   8
```

```
The invention relates to isolated nucleic acids encoding plant stress response proteins (including peptide-methionine sulphoxide response proteins (including peptide-methionine sulphoxide contents) as ABUSS148-ABUSS246 (or a protein 80% identical to them) from Zea mays, Oryza sativa, Glycine max, Or Triticum aestivum. Also included are expression cassettes, transformed host cells, cransgenic plants/seeds, modulating the level of peptide-methionine sulphoxide reductase in a plant and a computer system/dara processing system for identifying, analysing, or modelling a genetic sequence. The plant nucleic acid is useful in developing strategies to improve plant response to stress (e.g. drought, heat, radiation or pathogen attack), engineering plants with increased disease and stress cresistance, manipulating DNA repair and recombination efficiency, manipulating intracellular protein transport, and improving/protecting grain flavour. The nucleic acids may also be used as probes or cranscripts, for recombinant expression of encoded polypeptides, as immunogens in preparing or screening antibodies, and in sense or immunogens in preparing or screening antibodies, and in sense or continued antibodies specifically immunoreactive with the protein, and in assays continued protein antibodies specifically immunoreactive with the protein, and in assays or arragonists or antagonists.
                                                                                                                                                                                                                                                                     New peptide-methionine sulfoxide reductase and nucleic acids, useful in improving plant response to stress, engineering plants with increased disease and stress resistance, or and improving/protecting grain flavor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Odell JT, Rafalski JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila, developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.6%; Score 41; DB 24; Length 132; 50.0%; Pred. No. 28; tive 1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster polypeptide SEQ ID NO 27570.
    Miao G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     stress response protein (or fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB66926 standard; Protein; 1012 AA.
Meyers BC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97 EAAPPTTTAAEAPAIAAA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 2; 205pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 EEKTPLTTAAXAPVVXNA 19
                                                Weng Z;
```

ó

```
The present invention relates to the genome sequence of Listeria monocytogenes ED-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins carpeased from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and to hiosynthesis and biodegradation, especially biosynthesis of Vitemin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes related diseases. In addition, the genome caquence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                        Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49.4%; Score 40; DB 23; Length 258; 57.1%; Pred. No. 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klebsiella pneumoniae cellular proliferation protein #96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense, prokaryotic cellular proliferation protein, antibiotic, antibacterial, drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                           Claim 6; SEQ ID No 1187; 192pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zyskind JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU36108 standard; Protein; 445 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-191078P.
2000US-206848P.
2000US-207727P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-2001; 2001WO-US09180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158 EETELTNAVYAPVI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 EKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohlsen KL,
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klebsiella pneumoniae.
                                                                related polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-611495/70.
N-PSDB; AAS53967.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAY-2000; 2
23-OCT-2000; 2
27-NOV-2000; 2
22-DEC-2000; 2
16-FEB-2001; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haselbeck R,
Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU36108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
AAU36108
    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention suseful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dehoux P;
Cossart P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P, Checouani F, Nedjari H, Glaser P, Kunst F, Cossart P, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; ernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; T, Domann E, Hain T, Berche P, Charbit A, Durant L, J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibacterial; gene therapy, vaccine, biosynthesis, biodegradation, vitamin B12; bacterial infection; disease.
                                                                                                                                                                                                                                                                                                                                                                                                          insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
0
                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 27570; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Match 50.6%; Score 41; DB 22; Length 1012; Local Similarity 53.3%; Pred. No. 2.7e+02; les 8; Conservative 2; Mismatches 5; Indels (
                                                                                       Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Listeria monocytogenes protein #1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB48482 standard; Protein; 258 AA.
                                                                                       PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dussurger,
Daniels J, Goene,
Dominguez-Bernal G, Garrier,
Chakraborty T, Domann E, He
Perez-Diaz J, Baquero F, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         || || || :|:|
695 EEVTPYNTAPHSPIV 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-APR-2001; 2001WO-FR01118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-APR-2000; 2000FR-0004629.
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                       Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INSP ) INST PASTEUR.
                                                                                  Adams M,
                                                                                                                            WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-010914/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1012 AA;
                                          (PEKE ) PE CORP NY
                                                                                                                                                   N-PSDB; ABL11029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200177335-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Buchrieser C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-OCT-2001
                                                                                    Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB48482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB48482
```

g

ð

```
HIV-type retrovirus; MVP-5180/91; ECACC V 92092318; antigen; assay kit; detection; antibody; immune deficiency; vaccine.
                                                                           MVP-5180/91 has been isolated from peripheral lymphocytes of a patient, from the Cameroons, with immune deficiency. It grows in the same human cells as HIV-1; like HIV it produces an Mg-dependent reverse transcriptes (RT), although this is 3 to 7 kD smaller in Western blots than the enzyme from HIV-1 or -2. It is less reactive than HIV-1, but more reactive than HIV-2, against p24-specific antibodies and its gp41 transmembrane protein reacts with antibodies in sera of African patients but not (or only weakly) with sera of German patients.
                                                                                                                                                                                                                                                                     The virus consists of RNA in a peg-shaped core made of p24 subunits surrounded by an outer core of p17 and then a glycoprotein envelope which, apart from host-cell derived lipids, comprises gp41 and envelope protein gp120 (which can bind to the CD4 receptor). Related viruses have at least 75% homology over the entire genome with max. differences for the various regions LTR and NBF 10%, POL 12%, GAG 14%, VIF 15% and BNV 22%. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New HIV-type retrovirus and corresponding cDNA, recombinant DNA and antigen - used for detecting retro-viruses that cause immune deficiency and to prepare vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB 15; Length 498; Pred. No. 1.8e+02; 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Knapp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hauser H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guertler LG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW93076 standard; Protein; 498 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DADE-) DADE BEHRING MARBURG GMBH.
                                     Disclosure; Fig 7; 73pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 11; Fig 7; 39pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 EETSPROTSONYPIVTNA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92DE-4233646.
92DE-4235718.
92DE-4244541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIV isolate 5180 gag protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98EP-0114623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93DE-4318186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93EP-0116058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Conservative
infections and vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brunn AV, Eberle J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-072878/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              498 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-MAR-2003
19-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-0CT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP890642-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1993
05-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW93076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW9307
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococus aureus, Salmonella typhi, Klebsiella preumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The cinvention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to invention antibodies capable of binding to the expresse proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen car of the promotogous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

On the printed specification, but was obtained in electronic form part and promat directly from WIPO at sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus; HIV; antigen, detection; diagnosis; retrovirus; vaccine; lymphocyte; reverse transcriptase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .,
                      New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB 22; Length 445;
Pred. No. 1.6e+02;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New HIV-type immune deficiency virus ECACC V 92092318 - a deriv. cDNA or antigens, useful for diagnosing retroviral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Knapp S, Hauser H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIV-type virus MVP5180/91 gag protein (cloned).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIV-type virus MVP-5180/91 (ECACC V92092318)
                                                                                      Example 3; Seq ID No 11701; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brunn VA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR51691 standard; Protein; 498 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 57.1%;
Matches 8; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92DE-4235718.
92DE-4244541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92DE-4233646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93DE-4318186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93EP-0116058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                382 EQKTPLTAADMAAI 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 EEKTPLTTAAXAPV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Guertler LG, Eberle J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BEHW ) BEHRINGWERKE AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1994-120077/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAQ58974.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-OCT-1992;
30-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2003
07-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP591914-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR51691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
```

RESULT 15 AAR51691

셤

ò

.. 0

```
EM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB60583 standard; Protein; 788 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 EKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Li PWD,
                                                                                                                                                                                                                                                                                                                                                                             49.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198 EQTPLTTLRLAELIAEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                           8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-656860/75.
N-PSDB; ABL04686.
                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                      500 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Venter JC,
                                                                                                                                                                                                                                                                                          invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB60583;
                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in production of benzodiazephies, in particular anthramycin. The protein of encoded by the novel nucleic acid of the invention or a protein of 200 consecutive amino acids of that protein are useful for modifying a biological molecule that is a substrate for a polypeptide encoded by an anthramycin gene cluster. The anthramycin gene cluster present in a bacterium, preferably Escherichia coli strain DH10B having accession nos. IDAC 040602-1 and IDAC 040602-2, is useful for producing an anthramycin compound or anthramycin analogue. The genes and proteins provide the machinery for producing novel compounds based on the structure of anthramycins, and allow direct manipulation of anthramycin and related chemical structures via chemical engineering of the enzyme involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel isolated nucleic acid molecule involved
                    This invention describes the isolation of a novel HIV-type retrovirus called MPP-5180/91 (EACKC V 9209218). Antigens produced from this product can be used in an assay kit for detecting antibodies against viruses that cause immune deficiency, preferably where the assay is a Western blot. ELISA or fluorescence immunoassay. MVP-5180/91, cDNA and/or antigen can be used for detecting retroviruses that cause immune deficiency and to prepare vaccines. This sequence represents an HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful for directly manipulating benzodiazepines and related chemical structures by chemical engineering of enzymes involved in anthramycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acid involved in benzodiazepines production,
                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                          Score 40; DB 20; Length 498; Pred. No. 1.8e+02; 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Benzodiazepines biosynthesis protein SEQ ID No
                                                                                                                                                                                                PF field.)
PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Benzodiazepine; anthramycin; biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 14; Page 113-115; 166pp; English.
                                                                                                                                                                         MvP 5180 gag protein.
(Updated on 20-MAR-2003 to correct
(Updated on 20-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABJ37450 standard; Protein; 500 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                             | | : | |: |: | | | EETSPRQTSQNYPIVTNA 136
                                                                                                                                                                                                                                                                                                                                                                                                    19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ECOP-) ECOPIA BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                          49.4%;
ilarity 44.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JUN-2002; 2002WO-CA00864.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JUN-2001; 2001US-296744P.
                                                                                                                                                                                                                                                                                                                                                                                                 2 EEKTPLTTAAXAPVVXNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces refuineus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staffa A, Farnet CM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2003-156963/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (STAF/) STAFFA A.
(FARN/) FARNET C M.
                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                 498 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABT32131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2002101051-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            biosynthesis
                                                                                                                                                                                                                                                                                                                                                        .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                             119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABJ37450;
                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABJ37450
                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
************
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A PART A 
                                                                                                                                                                                                                                                                                                                                                                                                    à
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLioleth-ABLioli), expressed DNA sequences (ABLioleth-ABLioli), and the encoded proteins
biosynthesis of anthramycin, modifications which may not be presently sible by chemical methodology because of complexity of the structures. genes and proteins are also useful to introduce chemicals handles onormally inert positions that permit subsequence chemical
                                                                                                                                                                                        modification, achieving development of novel benzodiazepines, and generating a focused library of analogues around a benzodiazepine lead candidate to fine-tune the compound for optimal properties. The nucleic acids may be used as probes to identify and isolate DNAs encoding polypeptide sequences, and related nucleic acids. The nucleic acids useful for preparing the enzymes involved in the synthesis of anthramycine. The polypeptides are useful in a variety of biochemical reactions and for generating monoclonal or polyclonal antibodies. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ABBS7737-ABB72072).
The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence represents a benzodiazepines biosynthesis protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 8541; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40; DB 24; Length 500;
Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster polypeptide SEQ ID NO 8541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
```

Matches

SXS

RESULT 19 ABB6802

g Š

```
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ABB57737-ABB72072). The sequence data for this part of the printed The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 5631; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana protein fragment SEQ ID NO: 49147.
                                                                                                                                       Drosophila melanogaster polypeptide SEQ ID NO 5631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.8%; Score 39.5; DB 22; 52.6%; Pred. No. 9.1e+02; tive 3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myers EW;
                                 standard; Protein; 1793 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG39690 standard; Protein; 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 EEKTPLTT-AAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li PWD,
                                                                                                                                                                                                                                                                                                                                         23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 52.6
                                                                                                                                                                                                                                 Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1793 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                           (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABL03716
                                                                                                                                                                                                                                                                    WO200171042-A2
                                                                                                                                                                                               pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-OCT-2000
                                                                                                      26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG39690;
                                                                    ABB59613;
                                 ABB59613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 21
RESULT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG39690
                ABB59613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLi6176-ABL30511), expressed DNA sequences (ABLi6175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                          ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 30864; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22; Length 1473;
                                                                   Length 788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Indels
                                                                                                        7; Indels
                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster polypeptide SEQ ID NO 30864
                                                                    Score 40; DB 22;
Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40; DB 22
Pred. No. 6e+02;
2; Mismatches
 at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myers EW;
                                                                                                                                                                                                                                                                        ABB68024 standard; Protein; 1473 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
                                                                                                          1;
                                                                                                                                                                             602 EDGPTTTAAAAPLASAA 618
                                                                                                                                             13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.4%;
53.3%;
                                                                    n
Similarity 52.9%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-2001; 2001WO-US09231
                                                                                                                                         3 EKTPLTTAAXAPVVXNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adams M,
                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ABBS7737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1473 AA;
                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PEKE ) PE CORP NY
                                   788 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABL12127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                    pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interactions
                                                                                                                                                                                                                                                                                                                                           26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter JC,
                                                                                                                                                                                                                                                                                                           ABB68024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                       Sequence
```

ઠે d

ä

Gaps

;

Indels

Length 1793;

```
99US-0141842.
99US-0142154.
99US-0142355.
99US-0142390.
99US-0142803.
99US-0142920.
99US-0143542.
                                                                                                                 99US-0144005.
99US-0144085.
99US-0144086.
99US-0144335.
99US-0144331.
                                                                                                                                                                                                                                                                                                                             99US-0145145.
99US-0145218.
99US-0145224.
99US-0145913.
99US-0145913.
                                                                                                                                                                                                                                                                                                                                                                                           990S-0145919
990S-0145919
990S-0146386
990S-0146389
990S-0147308
990S-0147204
990S-0147302
990S-0147302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 990S - 0147416
990S - 0147416
990S - 0148171
990S - 0148171
990S - 0148181
990S - 01481841
990S - 0149186
990S - 0149172
990S - 0149723
990S - 0149723
990S - 0149723
990S - 0149920
990S - 0149930
990S - 0149930
990S - 0151066
                                                                                                                                                                                                                            99US-0144632.
99US-0144884.
99US-0144814.
99US-0145086.
                                                                                                                                                                                                                                                                       99US-0145088.
99US-0145085.
99US-0145087.
99US-0145089.
                                                                                                                                                                                            99US-0144334.
99US-0144335.
99US-0144352.
99US-0140991
                                                                                                                                                                                                                                                                                                                    99US-0145192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0137502
99US-0137724
99US-0138094
99US-0138540
99US-0139119
99US-0139119
99US-0139453
                                                                                            99US-0121825.
99US-0123180.
99US-0123180.
99US-0125788.
99US-0126785.
99US-0126785.
99US-0128714.
99US-0128714.
99US-0128714.
99US-013087.
99US-013087.
                                                                                                                                                                                                                                                                                                                 99US-0132487.
99US-0132863.
99US-0134218.
99US-0134219.
99US-0134219.
99US-0134370.
99US-0134768.
99US-0135124.
99US-0135124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0139750.
99US-0139763.
99US-0139817.
99US-0138899.
99US-0140353.
99US-0140354.
                                                                        25-FEB-2000; 2000EP-0301439
         Arabidopsis thaliana.
                             EP1033405-A2
                                                   06-SEP-2000
```

```
The invention relates to isolated polymuciecitie (1) and to polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques or restore normal activity of (II) is useful for generating antibodies against it, detecting or (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, foremaics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic amino acid sequences of the invention.

Commission acid sequences data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIFO expectives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yeast, protein-protein interaction, Selected Interacting Domain, SID (RTM); secretion yield; cancer, neurodegenerative disease; fungicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.1%; Score 39; DB 22; Length 137; 63.6%; Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yeast selected interacting domain protein SEQ ID NO: 636.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID No 56698; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABJ11251 standard; Protein; 159 AA.
                                                                                                      Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic; neuroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-FEB-2002; 2002WO-EP02299.
             31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-DEC-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |||||||: |:
104 TPLTTASATPL 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 TPLTTAAXAPV 15
                                                                                                          Drmanac RT, Liu C,
                                                                                                                                               WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 AA;
                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                 N-PSDB; AAS90526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200266504-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABJ11251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABJ11251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21; Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 59;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48.1%; Score 39;
66.7%; Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human diagnostic protein #26330.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG26339 standard; Protein; 137 AA.
                                                                       9903-0155139.
9903-0155486.
9903-0155659.
9903-0156596.
                                                                                                                                                                                                                                                                                                                      99US-0159295.
99US-0159329.
99US-0159330.
                                                                                                                                                                  99US-0157117.
99US-0157753.
99US-0157865.
99US-0158029.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0161920.
99US-0161992.
99US-0161993.
99US-0162142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                              99US-0158232
99US-0158369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0160815
99US-0160980
                                                                                                                                                                                                                                                                                                                                                                              99US-0159331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0160770
                                    99US-0154039
99US-0154779
                                                                                                                                                                                                                                                                                                    99US-0159294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0160814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 EKTPLTTAAXAP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EKPPSTTTASAP 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                    14-0CT-1999;
18-0CT-1999;
21-0CT-1999;
21-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG26339;
```

22-OCT-

RESULT 22

g

```
sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.
                                       cerevisiae polypeptides, comprising two Selected Interacting Domain (SID) polypeptides as bait and prey proteins. A pharmaceutical composition comprising the complex is useful for preventing or treating candida infection, cancer and neurodegenerative diseases in a human or animal, preferably in a mammal. This sequence represents a SID polypeptide of the
                 interacting Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yokoi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of nucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 17; SEQ ID NO: 5663; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                 Score 39; DB 23; Length 159;
Pred. No. 75;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ochiai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mizoguchi H, Ando S, Hayashi M,
Senoh A, Ikeda M, Ozaki A;
                          invention relates to a complex between two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glutamicum protein fragment SEQ ID NO: 5663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG91909 standard; Protein; 233 AA.
                                                                                                                                                                                                                                 48.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-DEC-2000; 2000EP-0127688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                            Query Match
Best Local Similarity 61...
Best Local Similarity 61...
                                                                                                                                                                                                                                                                                                                     2 EEKTPLTTAAXAP 14
                                                                                                                                                                                                                                                                                                                                                            14 EESTPPTATAAP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suropean Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corvneform bacterium:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-376931/40.
                                                                                                                                                                                          159 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAH67128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP1108790-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakagawa S,
Tateishi N,
                                                                                                                                                invention
                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG91909;
                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG91909
    ð
                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                The present invention relates to complexes between Saccharomyces cerevisiae Selected Interacting Domain (SID (RTM)) proteins and coding sequences. The protein complexes of S. cerevisiae are useful in drug development, in screening drugs or agents that modulate the interaction of proteins, for developing yeast strains with better secretion yield of protein, and in gene therapy. The protein complexes, polypeptides and polymucleotides are useful for preventing or treating Candida infection, cancer or neurodegenerative diseases in humans or animals. The present
                                                                                                                                                                                                         drug screening or development, for developing yeast strains with better secretion yield of protein, or in gene therapy (e.g. to treat Candida infection or cancer)
                                                                                                                                                                                      New protein-protein complexes of Saccharomyces cerevisiae, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New complex between two interacting bait and prey Saccharomyces cerevisiae polypeptides, useful for preventing or treating Candida infection, cancer or neurodegenerative diseases in a mammal -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 23; Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yeast; selected interacting domain; SID; antifungal; cytostatic; neuroprotective; Candida infection; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Selected Interacting Domain (SID) polypeptide #160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .,
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39; DB 2
Pred. No. 75;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence is a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG77349 standard; Protein; 159 AA.
                                                                                                                                                                                                                                                                                             Claim 6; Page 262; 357pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Page 127; 196pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.1%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JAN-2002; 2002WO-EP01350.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JAN-2001; 2001US-264577P.
16-FEB-2001; 2001US-269266P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 EEKTPLTTAAXAP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EESTPPTATAAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-619165/66.
N-PSDB; ABS62963.
                                                                                                                          WPI; 2002-674913/72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYBR-) HYBRIGENICS
                                       (HYBR-) HYBRIGENICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 AA;
                                                                                                                                              N-PSDB; ABT11568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200259255-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-2002
                                                                                 Legrain P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Legrain P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG77349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 24
```

à

XXXXXX

ž S

g ð

```
immunity against cancer. The compounds provided include polypeptides that contain at least one immunogenic portion of one or more SPAS-1 protein and DNA molecules encoding them or antigen obtained from transgenic adenocarcinoma mouse prostate (TRAMP)-C2 tumour cells. The immunogenic portion of the SPAS-1 human homologue polynucleotides sequence, SPAS-1 antibody or its antigen-binding fragment, the antigen-presenting cell, the T cell population and the pharmaceutical compositions are useful for inhibiting the development of a cancer in a patient, specifically prostate, breast, cervix, ovary, placenta, colon, brain, lung, kidney, chronic lymphocytic leukaemia or germ cell cancer. In particular, these compounds are useful as vaccines for inducing protective immunity against cancer. They are also useful for diagnosing cancer and monitoring cancer. They are also useful for diagnosing cancer and monitoring cancer progression. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prostate; breast; cervix; ovary; placenta; colon; brain; lung; kidney; chronic lymphocytic leukaemia; germ cell; vaccine; cytostatic; TRAMP; transgenic adenocarcinoma mouse prostate; mutant; mutein.
prostate, breast, cervix, ovary, placenta, colon, brain, lung, kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine; protective immunity; cancer; SPAS-1; T cell; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New SPAS-1 protein or antigen obtained from TRAMP-C2 tumor cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e capable of activating cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Wild-type Arg is substituted with His"
                                                                                                                                                                                                                                                                                                                                                                                                     Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                      The invention relates to compounds and methods for
                                                                                                                                                                                                                                                                                                                                                                                                      Score 39; DB 23;
Pred. No. 1.6e+02;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Antigenic epitope
TRAMP-specific murine T ce
                                                                                                                                                                                                                                                                                                                                  sequence is murine SPAS-1 partial protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine tumour SPAS-1 mutant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE22282 standard; Protein; 395 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shastri N;
                                                      English
                                                                                                                                                                                                                                                                                                                                                                                                        48.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-SEP-2001; 2001WO-US28621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-SEP-2000; 2000US-234472P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 SPITIAAIMPVV 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244..252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (REGC ) UNIV CALIFORNIA
                                                      Claim 2; Fig 1A; 107pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 TPLTTAAXAPVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fasso M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-362424/39.
N-PSDB; AAD35419.
                       or germ cell cancer
                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                        321 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200224739-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Allison JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus sp.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE22282;
                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE22282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
     ò
                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                            Murine, protective immunity; cancer, SPAS-1; T cell; pharmaceutical; prostate; breast; cervix; ovary; placenta; colon; brain; lung; kidney; chronic lymphocytic leukaemia; germ cell; vaccine; cytostatic; TRAMP;
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                          cancer; SPAS-1; T cell; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New SPAS-1 protein or antigen obtained from TRAMP-C2 tumor cells, useful as vaccine for treating or inhibiting cancer in patient, e.g.
                                                                                            ;
0
                                                        Length 233;
                                         Score 39; DB 22; Length 23.
Pred. No. 1.1e+02;
2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
Misc-difference 155...156
/note=_"Encoded by AGCTAAGCA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference 201..202
/note= "Encoded by TGCTAGTCC"
Misc-difference 204..205
/note= "Encoded by TTCTGACCT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            224..225
/note= "Encoded by ATTTGACAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239..240 '
/note= "Encoded by GCATGAAAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149..250
'note= "Encoded by GGTTGAGGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Encoded by TTCTAACTA"
Misc-difference 300..301
/note= "Encoded by TTCTGACCT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177..178
/note= "Encoded by ACCTAACCC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        by AAATAAATC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by GGATAAGGG"
                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                transgenic adenocarcinoma mouse prostate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Unknown
/note= "Encoded by AA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                      AAE22281 standard; Protein; 321 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shastri N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175..176
/note= "Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference 310..311
/note= "Encoded
                                                                                                                                                                                                                                                                                                                                                           Murine SPAS-1 partial protein.
                                                        48.1%;
nilarity 66.7%;
Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-SEP-2001; 2001WO-US28621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-SEP-2000; 2000US-234472P.
                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference 297..298
                                                                                                                              5 TPLTTAAXAPVV 16
                                                                                                                                                  35 TPTTSASPAPVV 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Allison JP, Fasso M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-362424/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 321
                                                                          Local Similarity
es 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAD35418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                         233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200224739-A2
                                                                                                                                                                                                                                                                                                                          25-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-MAR-2002
                                                                                                                                                                                                                                                                                        AAE22281;
                           Sequence
                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus sp.
                                                                             Best Loc
Matches
                                                                                                                                                                                                                     RESULT 26
                                                                                                                                                                                                                                    AAE22281
```

```
immunity against cancer. The compounds provided include polypeptides that contain at least one immunogenic portion of one or more SPAS-1 protein and DNA molecules encoding them or antigen obtained from transgenic adenocarcinoma mouse prostate (TRAMP)-C2 tumour cells. The immunogenic portion of the SPAS-1 human homologue polynucleotides sequence, SPAS-1 antibody or its antigen-binding fragment, the antigen-presenting cell, the T cell population and the pharmaceutical compositions are useful for inhibiting the development of a cancer in a patient, specifically prostate, breast, cervix, ovary, placenta, colon, brain, lung, kidney, chronic lymphocytic leukaemia or germ cell cancer. In particular, these compounds are useful as vaccines for inducing protective immunity against cancer. They are also useful for
                                                                                                                                                                    The invention relates to compounds and methods for inducing protective
  useful as vaccine for treating or inhibiting cancer in patient, e.g. prostate, breast, cervix, ovary, placenta, colon, brain, lung, kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosing cancer and monitoring cancer progression. The present sequence is murine tumour SPAS-1 mutant protein.
                                                                                                         Claim 2; Fig 1D; 107pp; English.
                                                       or germ cell cancer
####X#X
```

48.1%; 66.7%; 8; Conservative Query Match Best Local Similarity Matches

395 AA;

Sequence

ö

Gaps

;

DB 23; Length 395;

Score 39; DB 23; Lucia Pred. No. 2.1e+02; 300 SPTTTAATMPVV 311 5 TPLTTAAXAPVV 16 g ઠે

RESULT 28

AAE22283 standard; Protein; 395 AA. Murine normal SPAS-1 protein. (first entry) 25-JUL-2002

Murine; protective immunity; cancer; SPAS-1; T cell; pharmaceutical; prostate; breast; cervix; ovary; placenta; colon; brain; lung; kidney; chronic lymphocytic leukaemia; germ cell; vaccine; cytostatic; TRAMP; transgenic adenocarcinoma mouse prostate.

Mus ap

WO200224739-A2.

28-MAR-2002

21-SEP-2000; 2000US-234472P

13-SEP-2001; 2001WO-US28621.

(REGC) UNIV CALIFORNIA

ż

Shastri

Fasso M,

Allison JP,

WPI; 2002-362424/39. N-PSDB; AAD35420.

patient, e.g. 1, lung, kidney SPAS-1 protein or antigen obtained from TRAMP-C2 tumor cells, useful as vaccine for treating or inhibiting cancer in pa prostate, breast, cervix, ovary, placenta, colon, brain, or germ cell cancer New

Claim 2; Fig 1E; 107pp; English.

The invention relates to compounds and methods for inducing protective

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO

```
ö;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA. sequences (ABL01840-ABL30512) and the encoded proteins
            that contain at least one immunogenic portion of one or more SPAS-1 protein and DNA molecules encoding them or antigen obtained from transgenic adenocarcinoma mouse prostate (TRAMP)-C2 tumour cells. The immunogenic portion of the SPAS-1 human homologue polynuclectides sequence, SPAS-1 antibody or its antigen-binding fragment, the antigencempositions are useful for inhibiting the development of a cancompositions are useful for inhibiting the development of a cancomposition, specifically prostate, breast, cervix, ovary, placenta, colon, brain, lung, kidney, chronic lymphocytic leukaemia or germ cell ancer, in particular, these compounds are useful as vaccines for inducing protective immunity against cancer. They are also useful for diagnosing cancer and monitoring cancer progression. The present sequence is murine normal SPAS-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                      Gaps
polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, SEQ ID NO 30690; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                               Score 39; DB 23; Length 395;
Pred. No. 2.1e+02;
1; Mismatches 3; Indels
against cancer. The compounds provided include
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster polypeptide SEQ ID NO 30690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB67966 standard; Protein; 842 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PWD,
                                                                                                                                                                                                                                                                                               48.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                      8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           300 SPTTŤÁÁTMÞÝV 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ľ
                                                                                                                                                                                                                                                                                                                                                                       5 TPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                395 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABL12069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB67966;
                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 29
à
                                                                                                                                                                                                                                                                                                                                                                                                       g
```

Best Loc Matches

SXS

RESULT 30 ABB71511

a 8

```
the specification. The primer sets can be used in antisense therapy and the specification. The primers are useful for synthesising polymod-bottides, particularly full-length cDNAs. The primers are also useful for the sing polymod-bottides, particularly full-length cDNAs. The primers are also useful for the batch of the full-length cDNAs. The primers also useful for the full-length cDNAs. The primers allow obtaining of the full-length cDNAs assily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises a 1'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of oligonucleotide comprises at least 15 nucleotides and the combination of the comprise of the comprise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                         Human; primer; detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38; DB 22; Length 229;
Pred. No. 1.7e+02;
1; Mismatches 4; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saito K, Ya
, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; SEQ ID 15864; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hikawa T, Hayashi K, S
Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 EKTPLKTTATPLSPLKPPRMDTAPVVAS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 EKTPLTTAA-----XAPVVXN 18
                                                                                                                                                                                                             Human protein sequence SEQ ID NO:15864.
                                                 AAB94775 standard; Protein; 229 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ota T, Isogai T, Nishikawa
Ishii S, Sugiyama T, Wakama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JUL-1999; 99JP-0248036.
27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-JUN-2000; 2000JP-0241899
                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 39.3
les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229 AA;
                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                           EP1074617-A2
                                                                                                                                                        26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                             07-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                      AAB94775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
RESULT 31
                        AAB9477.
                                                                             pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
0
                                                                                                                                                              ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 41325; 21pp + Sequence Listing; English.
                                                                                                            Length 842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38; 'DB 22; Length 225;
Pred. No. 1.6e+02;
2; Mismatches 3; Indels
                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster polypeptide SEQ ID NO 41325.
                                                                                Score 38.5; DB 22;
Pred. No. 5.8e+02;
     at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                          ABB71511 standard; Protein; 225 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                                                                                                                                    598 EKTPIYSTTTKAPVVSTS 615
                                                                                                                                                                                                                  3 EKTPL-TTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.9%;
58.3%;
                                                                                                            47.5%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201 TPVTPAPTAPVI 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                  Local Similarity 50.0
les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 TPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 AA;
                                                          842 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ABL15614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Venter JC,
                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB71511;
                                                                                                               Query Match
```

ij

Gaps

ò 셤

```
The invention relates to novel human lung cancer polynucleotide (I) and polypeptides (II). (I) and (II) are useful in pharmaceutical compositions, such as vaccines, for the diagnosis and treatment of lung cancer. The polynucleotides are also useful as probes or primers for nucleic acid hybridisation. ABK24314-ABK24397 represent human lung cancer coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yokoi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                                                                                                New lung tumour polypeptides and polynucleotides, useful in pharmaceutical compositions, such as vaccines, for treating preventing lung cancer, or as probes or primers for nucleic hybridisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 46.9%; Score 38; DB 23; Length 229; Best Local Similarity 39.3%; Pred. No. 1.7e+02; Matches 11; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ochiai K,
                                                                                                                                                                                                                                       Switzer A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S, Hayashi M,
Ozaki A;
                                                                                                                                                                                                                                    Klee JI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 EKTPLKTTATPLSPLKPPRMDTAPVVAS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 EKTPLTTAA-----XAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C glutamicum protein fragment SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 8; Page 176; 179pp; English.
                                                                                                                                                                                                                                    Bangur CS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H, Ando S
Ikeda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG91455 standard; Protein; 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-DEC-1999; 99JP-0377484.
07-APR-2000; 2000JP-0159162.
                           25-MAY-2001; 2001WO-US17066.
                                                                                26-MAY-2000; 2000US-207485P.
06-SEP-2000; 2000US-230475P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-DEC-2000; 2000EP-0127688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000JP-0280988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mizoguchi
                                                                                                                                                                                                                                    Wang T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Senoh A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-376931/40.
                                                                                                                                                                          (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                            WPI; 2002-122068/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAH66674
                                                                                                                                                                                                                                 Harlocker SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP1108790-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakagawa
Tateishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG91455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 34
AAG91455
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARTY SERVICE STREET ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel polypeptide, double strand RNA joint zinc finger protein 25.19 and the polynucleotide encoding it. The polypeptide is useful in treating various diseases, such as embryo development malformation, tumours, immunological diseases and diabetes. The present invention also discloses the antagonist resisting the polypeptide and its treatment effect, and the application of the polynucleotides for encoding double strand RNA joint zinc finger protein 25.19. The sequence represents the zinc finger protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polypeptide-double strand RNA joint zinc finger protein 25.19 and polynucleotide encoding the polypeptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                        Double strand RNA joint zinc finger protein 25.19; tumour; diabetes; embryo development malformation; immunological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38; DB 23; Length 229;
Pred. No. 1.7e+02;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                             Double strand RNA joint zinc finger protein 25.19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; lung cancer; cytostatic; vaccine; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 28 (Disclosure); 34pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKTPLKTTATPLSPLKPPRMDTAPVVAS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---XAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq ID No 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BODE-) BODE GENE DEV CO LTD SHANGHAI.
                                                                                ABB81876 standard; Protein; 229 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU81227 standard; Protein; 229 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-AUG-2000; 2000CN-0119719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-AUG-2000; 2000CN-0119719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human lung cancer protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 39.3
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-455355/49.
N-PSDB; ABN86798.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 EKTPLTTAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200192525-A2
                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-APR-2002
                                                                                                                                                                                                  20-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU81227;
                                                                                                                                        ABB81876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
```

RESULT 33 AAU81227

d

ò

Mao Y,

```
recombination, of a promoter replacement fragment with a heterologous promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles of a gene are modified. The diploid fungal cells having both alleles modified are useful for identifying a gene that cells having both alleles modified are useful for identifying a gene that is essential to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian disease. (M1) is useful for identifying a compound which modulates the activity of a gene product, preferably enzymatic activity, carbon compound catabolism, biosynthetic, transporter, transcriptional, compound catabolism, biosynthetic, transporter, transcriptional, compound subolism biosynthetic, identifying a compound having the ability to inhibit growth or proliferation of C. albicans cells and for treating infection by C. albicans. The present sequence is that of an essential Candida albicans protein useful is not represented in the printed specification but is based on sequence information supplied to Derwent by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, DNA-binding protein, histone, chromo domain protein, chromatin organisation modifier, Y-box binding protein, DNA organisation, gene transcription, malignant disease, autoimmune disorder, rheumatic disease, genetic abnormality, infectious disease, neurological disorder, gene therapy, immunomodulatory, anti-HIV, anti rheumatic; anti microbial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38; DB 23; Length 276; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                           46.7%; Pred. No. 2007.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human DNA-binding protein #76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU18229 standard; Protein; 277 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0184664.
2000US-0186350.
2000US-0189874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0214886
2000US-0215135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUL-2000; 2000US-0216647.
07-JUL-2000; 2000US-0216880.
11-JUL-2000; 2000US-0217487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :||| | | :|: |
53 ETPLQTRAASPLTLN 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JAN-2001; 2001WO-US01305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0179065
2000US-0180628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-APR-2000; 2000US-0198123
19-MAY-2000; 2000US-0205515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-MAY-2000; 2000US-0205515
07-JUN-2000; 2000US-0209467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 KTPLTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0190076
                                                                                                                                                                                                                                                                                                                                                                                  the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 46.7 tes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      276 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200155162-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAR-2000; 2
16-MAR-2000; 2
17-MAR-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU18229;
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU18229
             ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                  The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacterium and identifying a homologue of a gene derived from coryneform bacterium. Coryneform saccharides and organic acids, particularly L-1ysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis; signal transduction; DNA replication; cell division; growth; proliferation; Candida albicans; fungicide; antifungal.
                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                 Claim 17; SEQ ID NO: 5209; 246pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 44; SEQ ID NO 7767; 167pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                    Score 38; DB 22; Length 261;
Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohlsen KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Candida albicans essential protein SEQ ID NO 7767.
                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bussey H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP73930 standard; Protein; 276 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boone C,
                                                                                                                                                                                                                                                                                                                                                                                      46.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-FEB-2001; 2001US-0792024. 22-AUG-2001; 2001US-314050P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-DEC-2001; 2001WO-US49486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-DEC-2000; 2000US-259128P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||||: :||
149 PLTTASASPV 158
                                                                                                                                                                                                                                                                                                         European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 PLTTAAXAPV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roemer T, Jiang B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-566694/60.
                                                                                                                                                                                                                                                                                                                                                 261 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB: ABZ32480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200253728-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP73930;
                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 35
                 ð
```

Gaps

ö

5; Indels

```
2000US-0224518.
2000US-0224519.
                                                                                                                                                                                                                                                                                                     2000US-0236369.
                                                                                    2000US-0226279
                                                                                                                                                                                                                                                                    2000US-0234998
                                                                                                     2000US-0227182
                                                                                                                                                                                                                                                                                                               2000US-0236370
                                                                                                                                                                                                                                                                                                                                               2000US-0239935
                                                              2000US-0225447
                                                                     2000US-0225757
                                                                                                                2000US-0228924
                                                                                                                          2000US-0229343
                                                                                                                                                                                                                                                                                                                                                                                                2000US-0241826
                                                                                                                                                                                                                                                          21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
                                                                                                                                                                                                                                                                                         29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
                                                                    14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
18-AUG-2000;
                                                                                                         23-AUG-2000;
                                                                                                                                                     06-SEP-2000;
                                                                                                                                                                                                                    14-SEP-2000;
                                                                                                                                                                                                                                                                               27-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                         20-OCT-2000;
20-OCT-2000;
                                                                                                                               01-SEP-2000;
                                                                                                                                                                                                                               14-SEP-2000;
                                                                                                                                                                                                                                                                          26-SEP-2000;
                                                                                                                                                                                                                                                     21-SEP-2000;
                                                                                                                                                                                          08-SEP-2000;
                                                                                              22-AUG-2000
22-AUG-2000
                                                                                                                                                                                                                                         14-SEP-2000
                                                                                                                                                                                                                                                                                                                                          02-OCT-2000
13-OCT-2000
                                                                                                                                                                          08-SEP-2000
                                                                                                                                                                                     08-SEP-2000
                                                                                                                                                                                                     12-SEP-2000
                                                                                                                                                                                                         14-SEP-2000
                                                                                                                                                                                                                                                                                                                    02-OCT-2000
02-OCT-2000
                                                                                                                                                                                                                                                                                                                                     02-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                    20-OCT-2000
                                                                                                                                               05-SEP-2000
                                                                                                                                                          06-SEP-2000
                                                                                                                                                               08-SEP-2000
                                                                                                                                                                     08-SEP-2000
                                                                                                                                                                                                                                                                                                                               02-OCT-2000
```

2000US-0246474. 2000US-0246475. 2000US-0246476. 2000US-0246477. 2000US-0246478. 2000US-0246524. 2000US-0246525. 2000US-0246526. 2000US-0246528 2000US-0246528 2000US-0246532 2000US-0246619 2000US-0246610 2000US-02466113 2000US-0249207. 2000US-0249208. 2000US-0249209. 2000US-0249210. 2000US-0249211. 2000US-0249212. 2000US-0249213. 2000US-0249213. 2000US-0249216 2000US-0249217 2000US-0249215 2000US-0249218 2000US-0249245 2000US-0249264 2000US-0249265 2000US-0249299 2000US-0249300 2000US-0251030 2000US-0251988 2000US-0251868 2001US-0259678 2000US-0249244 2000US-0250391 2000US-025409 08-NOV-2000; 17-NOV-2000; 01-DEC-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000 17-NOV-2000 01-DEC-20

Barash SC, Ruben SM; HUMA-) HUMAN GENOME SCI INC WPI; 2001-465557/50. Rosen CA,

Nucleic acid molecules encoding human secreted chromosomal binding proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers -N-PSDB; AAS29105

Claim 11; SEQ ID, No 214; 561pp; English.

The present invention relates to the isolation of novel DNA-binding proteins, and cDNA (AAS29130-AAS29157) and genomic sequences encoding for these proteins. DNA-binding proteins such as histones, chromo (chromatin organisation modifier) domain proteins, and Y-box binding proteins may contribute to diseases resulting from aberrant. DNA organisation and/or gene transcription. The sequences of the invention are useful in screening assays to identify antagonists and/or agonists that may enhance or block activities mediated by DNA-binding proteins. Blockers of DNA-binding proteins may be useful in treating disorders such as malignant diseases (e.g. cancer), autoimmune disorders

```
ö
                                                                                                                                                                                                                                                                                                                             Human; DNA-binding protein; B cell immunodeficiency; autoimmune disorder; severe combined immunodeficiency; rheumatoid arthritis; Crobn's disease; diabetes mellitus; allergy; asthma; inflammatory condition; thrombosis; graft-versus-host disease; blood-related disorder; atherosclerosis;
                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                 hyperproliferative disorder, cancer; renal disorder, arrhythmia; acute glomerulonephritis; cardiovascular disorder; respiratory disorder; Goodpasture's syndrome; neurological disorder; Alcheimer's disease; Parkinson's disease; medocrine disorder; Addison's disease; reproductive system disorder; endometriosis; infectious disease; viral infection; bacterial infection; fungal infection; vaccine; gastrointestinal disorder; multiple sclerosis; gene therapy.
                                                                                                                                                Gaps
(e.g. diabetes mellitus), rheumatic diseases (e.g. rheumatoid arthritis), genetic abnormalities (e.g. cystic fibrosis), infectious diseases (e.g. HIV) and neurological disorders (e.g. Alzheimer's disease). The polymucleotide sequences of the invention may also be used in gene therapy. AAU18154-AAU18281 represent novel DNA-binding
                                                                                                                                                .;
0
                                                                                                                           46.9%; Score 38; DB 22; Length 277;
46.7%; Pred. No. 2.18+02;
iive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                            ABG92650 standard; Protein; 277 AA.
                                                                                                                                                                                                                                                                                                          Human DNA-binding protein #76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-220963P
2000US-220964P
2000US-224518P
2000US-225567P
2000US-225268P
2000US-225268P
2000US-225268P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-180628P.
2000US-214886P.
2000US-216647P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-216880P.
2000US-217487P.
2000US-217496P.
2000US-218290P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-228924P.
2000US-229287P.
2000US-229343P.
                                                                                                                                                                                         120 TPVRPAASPIVSGA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-225447P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JAN-2001; 2001US-0764846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-226868P
                                                                                                                                                                     5 TPLTTAAXAPVVXNA 19
                                                                                                                    Query Match
Best Local Similarity 46.77
Conservative
                                                                                                                                                                                                                                                                                     18-NOV-2002 (first entry)
                                                                                                         277 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2002102638-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JUL-2000; 2
11-JUL-2000; 2
14-JUL-2000; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-2002
                                                                                                                                                                                                                                                                  ABG92650;
                                                                                                           Sequence
                                                        proteins
                                                                                                                                                                                                                         RESULT 37
                                                                                                                                                                                                                                                                 888888888888888
                                                                                                                                                                                          g
                                                                                                                                                                        ò
```

```
The present invention relates to a new DNA-binding protein. The invention is useful in treating, preventing, diagnosing and/or prognosing immunodeficiencies (e.g. B cell immunodeficiencies, severe combined immunodeficiencies), evere combined immunodeficiencies), autoimmune disorders (theumatoid arthritis, multiple confined disorders mellitus), allergic reactions and conditions (e.g. asthma), inflammatory conditions, graft-versus-host disease, bloodcortelates (thrombosis, atheroscierosis), hyperproliferative disorders (e.g. cancer), renal disorders (e.g. acute glomerulonephritis), cardiovascular disorders (e.g. arrhythmia), respiratory disorders (Goodpasture's syndrome), neurological disorders (e.g. Alzheimer's disease, Parkinson's disease), endocrine disorders (e.g. Alzheimer's disease), infectious diseases (e.g. viral, bacterial or fungal infections) and cuseful to stimulate neuronal growth and treat, prevent, and/or diagnose cuseful to stimulate neuronal growth and treat, prevent, and/or diagnose cuseful to stimulate neuronal growth and treat, prevent, and/or diagnose cuseful to stimulate neuronal growth and treat, prevent, and/or diagnose cuseful to stimulate physical present amino acid sequence represents a chuman DNA-binding protein of the invention.

Chuman DNA-binding protein of the invention.

Chuman DNA-binding protein of the invention.

Chuman premo, at premo, but was obtained in electronic format directly fermingent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel DNA-binding protein useful for diagnosis, prognosis, prevention and treatment of immune, hyperproliferative, respiratory, cardiovascular, reproductive, endocrine, gastrointestinal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.9%; Score 38; DB 23; Length 277;
46.7%; Pred. No. 2.1e+02;
ive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; SEQ ID No 214; 225pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http.seqdata.uspto.gov/sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barash SC;
                                                                                                                                                                                                                               2000US-236368P.
2000US-236369P.
                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-237040P.
2000US-239935P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-244617P.
2000US-249299P.
                                                                                                               2000US-234997P.
                                                                                                                                                                      2000US-236327P.
2000US-236367P.
                                                                                                                                                                                                                                                                                                                                                   2000US-237037P.
                                                                                                                                                                                                                                                                                                                                                                           2000US-237038P.
2000US-237039P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-240960P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-241809P.
                                                                                                                                              2000US-235834P
                                                                                                                                                                                                                                                                                         2000US-236370P
                                                                                                                                                                                                                                                                                                                    2000US-236802P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-241785P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-251856P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 46.7,
7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neurological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-690611/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ROSEN C A.
RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ABS68245.
                        08-SEP-2000;
21-SEP-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                        02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                   02-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-OCT-2000;
01-NOV-2000;
                                                                                                                                              27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-OCT-2000;
20-OCT-2000;
                                                                                                                      25-SEP-2000;
                                                                                                                                                                                                       29-SEP-2000;
                                                                                                                                                                                                                                                                                            29-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L7-NOV-2000;
05-SEP-2000;
                                                                                                                                                                                                                                      29-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rom USPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (RUBE/) H
(BARA/) H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ROSE/)
```

RESULT 38

ò

```
Avilamycin; antibacterial; virucide; protozoacide; fungicide; infection; medicine; Staphylococcus aureus; biosynthetic gene cluster; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces viridochromogenes Avi gene cluster polypeptide frame 1.
                                                                                    Retro virus; vector; aldehyde-dehydrogenase;
glutamylorysteine-synthetase; hematopoietic cell; cyclophosphamide;
chemotherapy; transgenic animal; gene therapy; cancer therapy;
selectable marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A novel retro virus vector encodes human cytosolic aldehydedehydrogenase and/or human glutamylcysteine-synthetase (AAR63673). Hematopoietic cells transfected by the vector are resistant to cyclophosphamide, providing a means of gene therapy that allows higher doses of toxic drugs to be used in cancer chemotherapy. The human genes may also be used as selectable markers for mammalian cell transfection and for transgenic animal breeding. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Retroviral vectors encoding human cytosolic aldehyde dehydrogenase or glutamyl cysteine synthetase - used to transform a subject's haematopoietic cells to reduce the toxic effects of cyclo phosphamide chemotherapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38; DB 15; Length 521;
Pred. No. 4.1e+02;
3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB98398 standard; Protein; 19938 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig.4; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||:|||| | :: |
215 EEQTPLTALHVASLIKEA 232
                                                                                                                                                                                                                                                                                                                                                        (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces viridochromogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 EEKTPLTTAAXAPVVXNA 19
                                                   Aldehyde-dehydrogenase Aldh-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.48;
                                                                                                                                                                                                                                                                                                                       93US-0041722.
                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                         Dallafavera R, Gianni A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Conservative
   (nbdated)
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1994-333177/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         521 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ72450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200268436-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-MAR-2003
                                                                                                                                                                                                                                                                                                                     01-APR-1993;
25-MAR-2003
08-MAY-1995
                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                WO9423015-A1
                                                                                                                                                                                                                                                 13-OCT-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB98398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BXBXGXEXBXBXGXG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The PLD gene was expressed in E. coli and the product shown to have sphingomyelinase activity.

The toxin can be used in the prepn. of vaccines for immunising sheep against caseous lymphadenties. The toxin may also be used in immunoassays for detection of antibody in diagnosis of CLA in sheep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterium pseudo-tuberculosis phospholipase toxin purificn. - by concn. crude toxin by ultrafiltration followed by chromatography on cation exchange resin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
0
                                                                                                                                                                                                                                                                                                                                                                                                              18..47
/label=identified by sequencing purified PLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.9%; Score 38; DB 11; Length 307; llarity 61.5%; Pred. No. 2.3e+02; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eggleton DG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                     Phospholipase D toxine gene; vaccine; diagnosis; PLD; caseous lymphadenitis; CLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IT, Hodgson ALM, Bird PI, Cox JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (COMW ) COMMONWEALTH SERUM LAB COMMISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Fig 4(A-C); 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR63672 standard; Protein; 521 AA.
                                                                                                                                        AAR07361 standard; protein; 307 AA.
                                                                                                                                                                                                                                                                                                                                                        Corynebacterium pseudotuberculosis.
                                                   120 TPVRPAASPIVSGA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89AU-0003422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90WO-AU00121
                                                                                                                                                                                                              (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 PLTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVGNAAAAPVVHN 30
                    TPLTTAAXAPVVXNA
                                                                                                                                                                                                                                                                   Phospholipase D toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1990-320256/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      307 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAQ06249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9011351-A.
                                                                                                                                                                                                            25-MAR-2003
31-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-OCT-1990
                    'n
                                                                                                                                                                             AAR07361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR63672
                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nisbet
```

ô

Gaps

; 0

RESULT 39

ò

AAR63672

```
Weitnauer G, Muehlenweg A, Trefzer A, Bechthold A;
                         (COMB-) COMBINATURE BIOPHARM AG.
    24-AUG-2001; 2001WO-EP09815.
              25-FEB-2001; 2001DE-1009166.
                                              WPI; 2003-018650/01.
N-PSDB; ABZ37515.
```

The invention relates to avilamycin derivatives (I) with antibacterial, virucide, protozoacide and fungicide activity. (I) are useful for reatment of infections (bacterial, viral, protozoal or fungal), in human or veterinary medicine, particularly where caused by Staphylococcus aureus. (I) are more hydrophilic than known avilamycins. The present sequence is that of an avilamycin synthesis enzyme from the Streptomyces viridochromogenes Avilamycin A biosynthetic gene cluster (ABZ37515-ABZ37516). New avilamycin derivatives, useful for treatment of infections, and nucleic acid encoding avilamycin synthesis enzymes Example 1; Page 68-301; 319pp; German.

Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative 5 TPLTTAAXAPVV 16

19938 AA;

Sequence

ö

0; Gaps

Score 38; DB 24; Length 19938; Pred. No. 2.4e+04; 2; Mismatches 3; Indels 0

Search completed: January 28, 2004, 13:08:11 Job time : 42 secs

|| :| | |||: 15995 TPASTRAAAPVI 16006 ð g

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

- protein search, using sw model

January 28, 2004, 13:07:24 ; Search time 21 Seconds (without alignments) 38.281 Million cell updates/sec

US-09-359-426C-2 81 Title: Perfect score:

1 XEEKTPLTTAAXAPVVXNA 19 Sequence:

Scoring table:

328717 segs, 42310858 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

328717 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents AA: Database :

/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

| Description | Sequence 21327, A | 12, | Ŋ | 59, | 59, | 59, | 59, | 59, | 59, | | 7139 | 5791 | Sequence 19222, A | Sequence 20, Appl | Sequence 20, Appl | | Sequence 4, Appli | | | | | 19, | 19, | 19, | 48 | 48, | Sequence 3558, Ap |
|--------------------------|----------------------|------------------|------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|--------------------|---------------------|----------------------|-------------------|-------------------|------------------|-------------------|-----------------|---------|-----------------|----------------------|------------------|------------------|------------------|------------------|------------------|---------------------|
| ID | US-09-252-991A-21327 | US-08-194-338-12 | - 1 | US-08-471-770-59 | US-08-468-059-59 | US-09-109-916-59 | US-09-886-156-59 | US-09-886-149-59 | US-09-886-150-59 | US-09-886-159-59 | US-09-328-352-7139 | US-09-107-532A-5791 | US-09-252-991A-19222 | US-08-624-125-20 | US-08-937-155-20 | US-08-679-635A-4 | US-09-419-163-4 | US-08-943-173-8 | -08-943 | US-08-943-173-2 | US-09-252-991A-17602 | US-09-117-257-19 | US-08-945-476-19 | US-09-489-352-19 | US-09-117-257-48 | US-09-489-352-48 | US-09-134-001C-3558 |
| DB | 4 | Н | Н | н | ~ | ٣ | 4 | 4 | 4 | 4 | 4 | 4 | 4 | Н | 4 | 7 | 4 | m | ო | ٣ | 4 | m | ო | 4 | m | 4 | 4 |
| Query Match Length DB | 482 | 788 | 49 | 498 | 498 | 498 | 498 | 498 | 498 | 498 | 145 | 262 | 342 | 456 | 456 | 463 | 463 | 19 | 58 | 71 | 162 | 181 | 181 | 181 | 182 | 182 | 236 |
| Query | 77.8 | 50.6 | 49.4 | 49.4 | 49.4 | 49.4 | 49.4 | 49.4 | 49.4 | 49.4 | 48.1 | 45.7 | 45.7 | 45.7 | 45.7 | 45.7 | 45.7 | 44.4 | 44.4 | 44.4 | 44.4 | 44.4 | 44.4 | 44.4 | 44.4 | 44.4 | 44.4 |
| Score | 63 | 41 | 40 | 40 | 40 | 40 | 40 | 40 | 40 | 40 | 39 | 37 | 37 | 37 | 37 | 37 | 37 | 36 | 36 | 36 | 36 | 36 | . 36 | 36 | 36 | 36 | 36 |
| Result No. | 1 | 7 | e | 4 | Ŋ | 9 | 7 | 80 | σ | 10 | 11 | 12 | 13 | 14 | 15 | .16 | 17 | . 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 |

| | ١ | | | | | | | | | | | | | | | | |
|------------------|-----------------|-----------------|-------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|--------------------|----------------------|----------------------|-----------------|-------------------|-------------------|-------------------|-------------------|
| | - | Appli | Appl | Appli | Appli | Appl | Appl | Appl | Appl | , App | 10, A | 21, A | Appli | App, | | , App | , App |
| 9 | 9 | ~ | 51, | 9 | , | 11, | 11, | 24, | 24, | 461, | 26910 | 32221 | 4, | 204 | 142 | 137 | 142 |
| Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence |
| | | | `, | | | | | | | | | | | | | | |
| US-09-446-301A-6 | US-09-099-932-6 | US-08-458-555-2 | US-09-446-301A-51 | US-07-821-717B-6 | US-08-119-262B-6 | US-08-135-929A-11 | US-08-234-265A-11 | US-09-091-219-24 | US-09-660-541-24 | US-08-936-165A-461 | US-09-252-991A-26910 | US-09-252-991A-32221 | US-09-009-816-4 | US-09-071-035-204 | US-08-818-112-142 | US-08-818-111-137 | US-09-056-556-142 |
| 4 | 4 | N | 4 | Н | ч | 7 | Н | М | 4 | 4, | 4 | 4 | 4 | 4 | ٣ | 4 | 4 |
| 294 | 295 | 355 | 507 | 610 | 610 | 610 | 610 | 2318 | 2318 | 136 | 181 | 185 | 223 | 225 | 267 | 267 | 267 |
| 4. | 4. | 4. | 4. | 4. | 4. | 4. | 4. | 4. | 4. | ۲. | ۲. | ۲. | 7 | 7 | 13.2 | 13.2 | 7 |
| 44.4 | 44 | 44 | 44 | 44 | 44 | 44 | 44 | 44 | 44 | 43.2 | 43 | 43 | 43 | 43 | 43 | 43 | 43 |
| 36 | 36 | 36 | 36 | 36 | 36 | 36 | 36 | 36 | 36 | 35 | 35 | 35 | 35 | 35 | 32 | 35 | 35 |
| 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |
| | | | | | | | | | | | | | | | | | |

ALIGNMENTS

```
Sequence 21327, Application US/09252991A
Sequence 21327, Application US/09252991A
Patent No. 6551795
GREERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ASERCIENCE: 107196.138
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PLING DATE: 1998-02-18
PRIOR PLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 63; DB 4; Lengtn 402.
Pred. No. 0.0075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 77.8%;
Best Local Similarity 82.4%;
Matches 14; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 EEKTPLTTAAXAPVVXN
US-09-252-991A-21327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-252-991A-21327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
```

ADDRESSEE: Knobbe, Martens, olson and Bear STREET: 620 Newport Center Drive, Sixteenth Floor CITY: Newport Beach US-08-194-338-12
| Sequence 12, Application US/08194338 |
| Patent No. 5474898 |
| Patent No. 5474898 |
| Patent No. 5474898 |
| APPLICANT: Venter, John C. |
| APPLICANT: Wencer, Claire M. |
| APPLICANT: McCombie, William R. |
| TITLE OF INVENTION: OCTOPAMINE RECEPTOR |
| WUMBER OF SEQUENCES: 16 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSER: Knobee, Martens, olson and Bee |
| ADDRESSER: Knobee, Martens, olson and Bee |
| ADDRESSER: Rnobee, Martens, olson and Bee |
| ADDRESSER: Rnobee, Martens, olson and Bee | EEKTRLTTAAGAPVVDN qq

COUNTRY:

ZIP: 92660 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

```
Sequence 59, Application US/08471770
; Sequence 59, Application US/0847170
; Parent No. 5770470
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Guertler, Lutz G.
APPLICANT: Brunn, Albrecht v.
APPLICANT: Knapp, Stefan
; APPLICANT: Knapp, Stefan
; TITLE OF INVENTION: Retrovirus from the HIV Group and Its
; TITLE OF INVENTION: Use
; UNWBER OF SEQUENCES: 63
; CORRESPONDENCES. 63
; CORRESPONDENCES. 1000 NAME OF SEQUENCES. 1000 NAME 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 44.4%; Pred. No. 56;
Matches 8; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett ADDRESSEE: Dunner STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,770
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/132,653
FILING DATE: 05-OCT-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                         05495-0001-00000
APPLICATION NUMBER: DE P 42 35 718.7
FILING DATE: 22-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 42 44 541.8
FILING DATE: 30-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 18 186.4
FILING DATE: 01.-UNN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Michael J. Blake
REGISTRATION NUMBER: 37,096
REFERENCE/DOCKET NUMBER: 05495-0001-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 42 33 646.5
FILING DATE: 06-0C1-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 42 35 718.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 498 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 EETSPROTSONYPIVTNA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-470-202-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 59, Application US/08470202
Patent No. 5759808
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Eberle, Josef
APPLICANT: Knapp, Stefan
APPLICANT: Hanger, Stefan
APPLICANT: Hanser, Hans-Peter
IITLE OF INVENTION: Retrovirus from the HIV Group and Its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41; DB 1; Length 788;
Pred. No. 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner STREET: 1300 I Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,202
                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                      NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,655
REPERENCE/DOCKET NUMBER: NIH101.001DV1
TELECOMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
INFORMATION FOR SEQ 1D NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/132,653
FILING DATE: 05-0CT-1993
APPLICATION NUMBER: DE P 42 33 646.5
FILING DATE: 06-0CT-1992
                                                                                                               APPLICATION NUMBER: US/08/194,338
FILING DATE: 08-FEB-1994
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,174
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               602 EDOPTTTÄÄÄÄÄPLASÄÄ 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 EKTPLITAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 788 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 52.94
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Ret
TITLE OF INVENTION: USA
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ,ab.
D.C.
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ANTI-SENSE: NO
; FRAGMENT TYPE:
US-08-194-338-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-470-202-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: D
COUNTRY:
```

ò

```
49.4%; Score 40; DB 2; Length 498; 44.4%; Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49.4%; Score 40; DB 3; Length 498; 44.4%; Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 59, Application US/09109916
Patent No. 6277561
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Eberle, Josef
APPLICANT: Brunn, Albrecht V.
APPLICANT: Knapp, Stefan
APPLICANT: Hauser, Hans-Peter
TITLE OF INVENTION: RETROVING FROM HIV GROUP AND ITS USE
FILE REFERENCE: 05495.0001-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/109,916
CURRENT FILING DATE: 1980-07-02
EARLIER APPLICATION NUMBER: UB P 42 33 646.5
EARLIER FILING DATE: 1992-10-06
EARLIER APPLICATION NUMBER: UE P 42 35 718.7
EARLIER FILING DATE: 1992-10-22
EARLIER FILING DATE: 1992-10-22
EARLIER FILING DATE: 1992-10-20
EARLIER FILING DATE: 1992-12-30
EARLIER FILING DATE: 1993-06-01
EARLIER APPLICATION NUMBER: DE P 43 18 186.4
EARLIER PILING DATE: 1993-06-01
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PATENTIN UNET: 2.0
                                                                                                                                                                                       05495-0001-02000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 56;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
MBER: DE P 42 44 541.8
30-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Human immunodeficiency virus
         FILING DATE: 30-DEC-10--
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 18
FILING DATE: 01-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garol P. Einaudi
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 05499:
TELECOMMUNICATION INFORMATION:
TRIEPHONE: 202-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
US-02-886-156-59
'Sequence 59, Application US/09886156
; Patent No. 6528626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 EETSPRQTSQNYPIVTNA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 EETSPRQTSQNYPIVTNA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 5 SEQUENCE CHARACTERISTICS: LENGTH: 498 amino acids TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 44.43
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 44.4
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
FRAGMENT TYPE: internal
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
US-09-109-916-59
                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-468-059-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-109-916-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Guerlier, Lutz G.
APPLICANT: Bberle, Josef
APPLICANT: Brun, Albrecht v.
APPLICANT: Brun, Albrecht v.
APPLICANT: Hauge, Stefan
APPLICANT: Hauser, Hans-Peter
TITLE OF INVENTION: Retrovirus from the HIV Group and Its
TITLE OF INVENTION: Use
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Mashington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: ELADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,059
FILING DATE: 06-UNN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/132,653
FILING DATE: 05-OCT-1993
CLASSIFICATION: A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 42 33 646.5
FILING DATE: 06-OCT-1992
                                                                                                                                                                                  NAME: Carol P. Einaudi
REGISTRATION NUMBER: 32,220
REFERENCE, DOCKET NUMBER: 05495-0001-03000
TELECOMMINICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 42 44 541.8
FILING DATE: 30-DEC-1992
                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 18 186.4
FILLING DATE: 01-UUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Carol P. Einaudi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 59, Application US/08468059 Patent No. 5840480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           || :| |: |: || || || 119 EETSPRQTSQNYPIVTNA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 44.4%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-OCT-1992
22-OCT-1992
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 498 amino acids
                                                                                                                                                                                                                                                                                                         TELEFAX: 202-408-4400 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 06-OCT-:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ,ab.
D.C.
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-471-770-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
```

g

```
.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: EDEFIE, JOSEF
APPLICANT: EDEFIE, JOSEF
APPLICANT: Brunn, Albrecht V.
APPLICANT: Mangp, Steer
APPLICANT: Hans-Peter
APPLICANT: Hans-Peter
TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE
FILE REFERENCE: 05495, 0001-04
CURRENT APPLICATION NUMBER: US/09/886,159
CURRENT FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1992-10-06
PRIOR FILING DATE: 1992-10-06
PRIOR FILING DATE: 1992-10-22
PRIOR APPLICATION NUMBER: DE P 42 35 718.7
PRIOR FILING DATE: 1992-10-22
PRIOR PLING DATE: 1992-10-22
PRIOR PLING DATE: 1992-10-22
PRIOR PLING DATE: 1992-10-36
PRIOR FILING DATE: 1992-10-36
PRIOR FILING DATE: 1992-10-36
PRIOR FILING DATE: 1992-10-36
PRIOR FILING DATE: 1993-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 44.4%; Pred. No. 56;
Matches 8; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                APPLICANT: Brunn, Albrecht V.
APPLICANT: Knapp, Stefan
APPLICANT: Hauser, Hans-Peter
FILTLE OF INVENTION RETROVIRUS FROM HIV GROUP AND ITS USE
FILTE REFERENCE: 05495,0001-04
CURRENT APPLICATION NUMBER: US/09/886,150
CURRENT FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/109,916
PRIOR APPLICATION NUMBER: 09/109,916
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-10-06
PRIOR FILING DATE: 1992-10-06
PRIOR FILING DATE: 1992-10-22
PRIOR FILING DATE: 1992-10-22
PRIOR FILING DATE: 1992-10-22
PRIOR FILING DATE: 1992-10-23
PRIOR FILING DATE: 1992-10-30
PRIOR FILING DATE: 1993-06-01
PRIOR PRIOR DATE: 1093-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US-09-886-159-59
; Sequence 59, Application US/09886159
                                                                                                                         RESULT 9
US-09-886-150-59
; Sequence 59, Application US/0986150
; Patent No. 6531587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 EETSPROTSONYPIVTNA 136
                                119 EETSPROTSONYPIVTNA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                APPLICANT: Guertler, Lutz
APPLICANT: Eberle, Josef
                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-886-150-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
APPLICANT: Gueriler, Lutz G.
APPLICANT: Beerle, Josef
APPLICANT: Brunn, Albrecht V.
APPLICANT: Brunn, Albrecht V.
APPLICANT: Hauser, Hans-Peter
TITE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE
FILE REPERENCE: 05495.0001-04
CURRENT APPLICATION NUMBER: US/09/886,156
CURRENT APPLICATION NUMBER: US/09/106
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-06
PRIOR FILING DATE: 1992-10-06
PRIOR PILING DATE: 1993-10-07
PRIOR FILING DATE: 1993-06-01
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PATENTIN VET. 2.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: EDEFILE, JOSEE
APPLICANT: EDEFILE, JOSEE
APPLICANT: EDEFILE, JOSEE
APPLICANT: Hauser, Hans-Peter
APPLICANT: Hauser, Hans-Peter
TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE
FILE REFERENCE: 05495.0001.04
FILE REFERENCE: 05495.0001.04
CURRENT PILING DATE: 2001-06-22
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1992-10-06
PRIOR FILING DATE: 1992-10-22
PRIOR APPLICATION NUMBER: DE P 42 35 718.7
PRIOR FILING DATE: 1992-10-22
PRIOR APPLICATION NUMBER: DE P 42 44 541.8
PRIOR FILING DATE: 1992-12-30
PRIOR PILING DATE: 1993-06-01
NUMBER OF SEQ ID NOS: 67
SOFFWARE: PATENTING DATE: 1933-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
49.4%; Score 40; DB 4; Length 498;
Best Local Similarity 44.4%; Pred. No. 56;
Matches 8; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 49.4%; Score 40; DB 4; Length 498; Best Local Similarity 44.4%; Pred. No. 56; 7; Indels Matches 8; Conservative 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , ORGANISM: Human immunodeficiency virus US-09-886-156-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 59, Application US/09886149 Patent No. 6531137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 EETSPROTSONYPIVTNA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Guertler, Lutz G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-886-149-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-886-149-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 59
LENGTH: 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 59
LENGTH: 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

Gaps

Gaps

.. 0

```
APPLICANT: Marc J: Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 19222
LENGTH: 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20, Application US/08624125

Patent No. 5744341

GENERAL INFORMATION:
APPLICANT: CUNNINGHAM JR., FRANCIS X.
APPLICANT: SUN ZAIREN

ITILE OF INVENTION: METABOLISM AND A SYSTEM FOR SCREENING SUCH GENES

ITILE OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                              Length 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: P.C.
1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 4;
Pred. No. 1.2e+02
                                                                                                                                                                                                                                                                                                                                                                                            Score 37; DB 4;
Pred. No. 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...262
SEQUENCE DESCRIPTION: SEQ ID NO: 5791:
                                                                                                                                                                                                                            ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19222, Application US/09252991A
Patent No. 6551795
REFERENCE/DOCKET NUMBER:
                   TELECOMMUNICATION INFORMATION
                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 262 amino acids
TYPE: amino acid
                                                      TELEFAX: (781)893-8277
                                                                                INFORMATION FOR SEQ ID NO: 5791:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.7%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                            45.7%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 PVTPTAAAPVIDKA 293
                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 PLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 8/..
Best Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 EKTPLTTA 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 EKTPLTTS 19
                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION: APPLICANT: Marc J:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-252-991A-19222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-252-991A-19222
                                                                                                                                                                                                                                                                                                                                                   US-09-107-532A-5791
                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-08-624-125-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                    Sequence 7139, Application US/09328352

Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                            Gaps
                                                                                                                                            ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB 4; Length 145; Pred. No. 20;
                                                                                                   4; Length 498;
                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                 DB
56;
                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                               Query Match
Best Local Similarity 44.4%; Pred. No.
Matches 8; Conservative 3; Mismatc
                   ; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-886-159-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5791, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                           || :| |: || |: || || || 119 EETSPRQTSQNYPIVTNA 136
                                                                                                                                                                               2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66.7-
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 KTPLTTAAXAPV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 RMPLTAAAQAPV 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-107-532A-5791
                                                                                                                                                                                                                                                                                                          US-09-328-352-7139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-328-352-7139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 7139
LENGTH: 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                 ò
                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

ô

Gaps

.; 0

```
; Sequence 4, Application US/08679635A
; Patent No. 5985643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
          TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 456 amino acids
                                                                                                                                                                                                                45.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                               Query Match
Best Local Similarity 72.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              382 TTAAAAPLVQTA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 TTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : protein
NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                       336 TLAAAPVVANA 346
                                                                                       TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                 , MOLECULE TYPE: protein US-08-937-155-20
                                                                                                                                                                                                                                                                                               9 TAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-679-635A-4
                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 20, Application US/08937155
; Sequence 20, Application US/08937155
; Patent No. 6524811
; GENERAL INFORMATION:
    APPLICANT: CUNNINGHAM JR., FRANCIS X.
    APPLICANT: CUNNINGHAM JR., FRANCIS X.
    TITLE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND TITLE OF INVENTION: METABOLISM AND A SYSTEM FOR SCREENING SUCH GENES NUMBER OF SEQUENCES: 21
    CORRESPONDENCE ADDRESS: ADDRESSEE: P.C.
    STREST: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
    CITY: ARLINGTON
    STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB 1; Length 456; Pred. No. 1.6e+02;
                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/624,125
FILING DATE: 29-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRANT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: KELBER, STEVEN B.
REGISTRATION NUMBER: 30,073
REFENCE/DOCKET NUMBER: 2747-063-27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: KELBER, STEVEN B.
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 2747-063-27
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/624,125
FILING DATE: 29-WAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        TELEPAX: 703-413-2220
TELEPAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 456 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 72...
8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         336 TLAAAPVVANA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-08-624-125-20
                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
ARLINGTON
                                                                                                                                                                                                                    FILING DATE: 2 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                      22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-937-155-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
```

```
GENERAL INFORMATION:
APPLICANT: Tomasz, Alexander
APPLICANT: Delencastre, Herminia
TITLE OF INVENTION: AUXILIARY GENES AND PROTEINS OF
TITLE OF INVENTION: METHICILLIN RESISTANT BACTERIA AND ANTAGONISTS THEREOF
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.7%; Score 37; DB 2; Length 463; 66.7%; Pred. No. 1.6e+02;
Length 456;
                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37; DB 4; ]
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
TELEFENCE/DOCKET NUMBER: 600-1-141
TELEFORMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
```

```
Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEPTIDES DERIVED FROM THE NON-STRUCTURAL PROTEINS OF FOOT AND MOUTH DISEASE VIRUS AS DIAGNOSTIC REAGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36;
Pred. No.
                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,173
RILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lin, Maria C.H.
REGISTRATION NUMBER: 29,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10154-0053
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,173
FILING DATE:
COUNTRY: USA
ZIF: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 16, Application US/08943173 Patent No. 6048538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
APPLICANT: Shen, Fan, Fan
APPLICANT: Chen, Pei De
TITLE OF INVENTION: PEPTIDES D
TITLE OF INVENTION: FROM THE N
TITLE OF INVENTION: DIAGNOSTIC
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSES: MATIA C.H. Lin
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Lin, Maria C.H.
REGISTRATION NUMBER: 29,3
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 53.33,
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S EROKPLKVKAKAPVV 19
                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-943-173-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-943-173-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                 Sequence 4, Application US/09419163
Patent No. 6391614
GENERAL INFORMATION:
APPLICANT: Tomasz, Alexander
APPLICANT: Delencastre, Herminia
TITLE OF INVENTION: MUXILIARY GENES AND PROTEINS OF
TITLE OF INVENTION: METHICILLIN RESISTANT BACTERIA AND ANTAGONISTS THEREOF
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37; DB 4; Length 463;
Pred. No. 1.6e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEPTIDES DERIVED FROM THE NON-STRUCTURAL PROTEINS OF FOOT AND MOUTH DISEASE VIRUS AS DIAGNOSTIC REAGENTS
                                                                                                                                                                                                         ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/419,163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: JacKson EG,, David A.
REGISTRATION NUMBER: 26,742
REPERENCE/DOCKET NUMBER: 600-1-141
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPHAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/679,635
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
BDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/08943173
Patent No. 6048538
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: PEPTIDES I
TITLE OF INVENTION: FROM THE N
TITLE OF INVENTION: FOOT AND N
TITLE OF INVENTION: DIAGNOSTIC
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wang, Chang Yi
APPLICANT: Shen, Fan
APPLICANT: Chen, Pei De
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                463 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               382 TTAAAAPLVQTA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 TTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                   CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-943-173-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-419-163-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
```

0; Gaps

```
US-09-252-991A-17602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-117-257-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 23
US-08-945-476-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                               엄
                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 71;
                                                                                                                         Score 36; DB 3; Length 58;
Pred. No. 23;
1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           PEPTIDES DERIVED
FROM THE NON-STRUCTURAL PROTEINS OF
FOOT AND MOUTH DISEASE VIRUS AS
DIAGNOSTIC REAGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.4%; Score 36; DB 3;
llarity 53.3%; Pred. No. 29;
Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 17602, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1151-4152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lin, Maria C.H.
REGISTRATION NUMBER: 29,323
REFRENCE/DOCKET NUMBER: 1151.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-758-4800
                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08943173
Patent No. 6048538
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 71 amino acids
                                                                                                                                 Query Match
Best Local Similarity 53.3%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 ERQKPLKVKAKAPVV 45
                                                                                                                                                                                                           2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                             31 ERQKPLKVKAKAPVV 45
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wang, Chang Yi
APPLICANT: Shen, Fan
APPLICANT: Chen, Pei De
                 ; LENGTH: S8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-943-173-16
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: peptide US-08-943-173-2
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Chen, Pei
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: line-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-252-991A-17602
                                                                                                                                                                                                                                                                                                                       US-08-943-173-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                            ò
```

```
TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17602
LENGTH- 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Hook, Magnus
APPLICANT: Hook, Mark
APPLICANT: Hanson, Mark
TITLE OF INVENTION: Dbpa AND DbpB COMPOSITIONS AND METHODS OF USE
FILE REFERENCE: 4220 000500
CURRENT APPLICATION NUMBER: US/09/117,257
CURRENT FILING DATE: 1998-07-22
BARLIER APPLICATION NUMBER: 08/589,711
BARLIER PILING DATE: 1996-01-22
BARLIER FILING DATE: 1996-01-24
SARLIER PILING DATE: 1996-01-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19, Application US/08945476
; Patent No. 6248517
; GENERAL INFORMATION:
; TITLE OF INVENTION: DECORIN BINDING PROTEIN COMPOSITIONS AND TITLE OF INVENTION: METHODS OF USE
; NUMBER OF SEQUENCES: 27
; COMPUTER REALBABLE FORM:
; MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

44.4%; Score 36; DB 3; Length 181;
Best Local Similarity 47.1%; Pred. No. 83;
Matches 8; Conservative 1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36; DB 4; Length 162;
Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19, Application US/09117257
Patent No. 6214355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 EKTPTTTAEGIITIAKA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 EKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Borrelia afzelii
US-09-117-257-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 KTPLTTAAXAP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RTPAATAAIAP 11
```

Gaps

. 0

```
Sequence 3558, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hook, Magnus
APPLICANT: Hook, Magnus
APPLICANT: Guo, Betty
APPLICANT: Guo, Betty
TITLE OWN.
TITLE OWN.
TITLE OF INVENTION: DDDA AND DDDB COMPOSITIONS AND METHODS OF USE
FILE REPERENCE: 4210.000500
CURRENT APPLICATION NUMBER: US/09/489.352
CURRENT APPLICATION NUMBER: PCT/US96/17081
EARLIER FILING DATE: 1996-10-22
EARLIER FILING DATE: 1996-01-22
EARLIER APPLICATION NUMBER: 08/589,711
EARLIER PILING DATE: 1996-01-22
EARLIER APPLICATION NUMBER: 08/427,023
EARLIER PILING DATE: 1995-04-24
                                                                                                                                                                                                                                                                                                                                                                                                     Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 3;
Pred. No. 84;
                 CURRENT APPLICATION NUMBER: US/09/117,25/
CURRENT FILING DATE: 1998-07-22
EARLIER APPLICATION NUMBER: PCT/US36/17081
EARLIER FILING DATE: 1966-10-22
EARLIER FILING DATE: 1966-10-22
EARLIER APPLICATION NUMBER: 08/589,711
EARLIER APPLICATION NUMBER: 08/427,023
EARLIER FILING DATE: 1996-01-24
NUMBER OF SEQ ID NOS: 66
SOFWWARE: PATENTING DATE: 1995-04-24
NUMBER OF SEQ ID NOS: 66
SOFWWARE: PATENTING DATE: 1995-04-24
                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 84;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 48, Application US/09489352
Patent No. 6312907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 ÉKTPTTTÁEGIITIAKÁ 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 EKTPTTTAEGIITIAKA 155
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 47.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 EKTPLTTAAXAPVVXNA
                                                                                                                                                                                                                                                                                                                                  ORGANISM: Borrelia afzelii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Borrelia afzelii
US-09-489-352-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 27
US-09-134-001C-3558
                                                                                                                                                                                                                                                                                                                                                         US-09-117-257-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Hook, Magnus
APPLICANT: Guo, Betty
APPLICANT: Hanson, Mark
TITLE OF INVENITON: DbpA AND DbpB COMPOSITIONS AND METHODS OF USE
FILE REFERENCE: 4210.000500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hook, Magnus
APPLICANT: Guo, Betty
APPLICANT: Hanson, Mark
TITLE OF INVENTION: DbpA AND DbpB COMPOSITIONS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Indels
                                         PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/489,352
CURRENT FILING DATE: 2000-01-21
EARLIER APPLICATION NUMBER: PCT/US96/17081
EARLIER FILING DATE: 1996-10-22
EARLIER FILING DATE: 1996-01-22
EARLIER PILING DATE: 1996-01-22
EARLIER APPLICATION NUMBER: 08/59,711
EARLIER PILING DATE: 1996-01-22
EARLIER FILING DATE: 1996-01-22
EARLIER FILING DATE: 1995-04-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36;
Pred. No.
                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/589,711
FILING DATE: 22-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/427,023
FILING DATE: 24-APPL-1995
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,476
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19, Application US/09489352
Patent No. 6312907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 48, Application US/09117257
Patent No. 6214355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 EKTPTTAEGIITIAKA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139 EKTPTTAEGIITIAKA 155
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 EKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 EKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.48;
47.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.48;
47.18;
                                                                                                                                                                                                                                                                                                                                : 181 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 47.13
Best Local Similarity 47.13
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT

ORGANISM: Borrelia afzelii

US-09-489-352-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 47.13
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -09-117-257-48
                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -09-489-352-19
                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-945-476-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
```

Indels

```
Gaps
                      ..
0
                                                                                                                                                                                                                   Sequence 2, Application US/08458555
Patent No. 5840689
GENERAL INFORMATION:
APPLICANT: Daniloff, Joanne K
APPLICANT: Daniloff, Joanne K
APPLICANT: Meintjes, Elmarie
TITLE OF INVENTION: Method for Stimulating the Regrowth of
TITLE OF INVENTION: Neurons
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 2; Length 355; Pred. No. 1.8e+02;
                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Attorney No. 5840689 9312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,555
  61.5%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 08/146,734
FILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Runnels, John H
REGISTRATION NUMBER: 33451
REPERENCE/POCKET NUMBER: Attorney N
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 31
US-09-446-301A-51
US-09-446-301A-51
Sequence 51, Application US/09446301A
Patent No. 6506893
GENERAL INFORMATION:
APPLICANT: EL SOLH, NEVINE
APPLICANT: ALLIGNET, JEANINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 70821-2471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                      3E: John H. Runnels
P. O. Box 2471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308 ETTPLTEPEKAPV 320
                                                                                                          174 EEYPLPTNAAAPV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 EKTPLITAAXAPV 15
                                                               3 EKTPLTTAAXAPV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 504 346-8049 INFORMATION FOR SEQ ID NO:
Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAM. TOPOLOGY: linear MOLECULE TYPE: protein TYPE: Drotein
                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: P. O. box CITY: Baton Rouge
                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                     US-08-458-555-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-458-555-2
                                                                                                                                                                              RESULT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                            g
                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/09446301A;
Sequence 6, Application US/09446301A;
Patent No. 6506893
GENERAL INFORMATION:
APPLICANT: EL SOLH, NEVINE
TITLE OF INVENTION: POLYNUCLEOTIDES AND THEIR USE FOR DETECTING RESISTANCE
TITLE OF INVENTION: POLYNUCLEOTIDES AND THEIR USE FOR DETECTING RESISTANCE
TITLE OF INVENTION: OCMPONING
FILE REFERENCE: 03715-0059
CURRENT FILING DATE: 1999-12-20
NUMBER OF SEQ ID NOS: 51
SEQ ID NO 6
LENGTH: 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-039-932-6

Sequence 6, Application US/0909932

Jatent No. 6570001

Jatent No. 6570001

Jatent No. 6570001

JAPLICANT: El Solh, Nevine

APPLICANT: Allignet, Jeanine

TITLE OF INVENTION: POLYNUCLEOTIDES AND THEIR USE FOR DETECTING RESISTANCE

TITLE OF INVENTION: TO STREPTORAMIN A OR TO STREPTOGRAMIN B AND RELATED

TITLE OF INVENTION: COMPOUNDS

TITLE OF INVENTION: COMPOUNDS

TITLE REFERENCE: 03495.0173-00000

CURRENT APPLICATION NUMBER: US/09/099,932

CURRENT FILING DATE: 1998-06-19

EARLIER APPLICATION NUMBER: 60/050,380

EARLIER FILING DATE: 1997-06-20

NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 4; Length 294;
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 295;
                                                                                                                                                                                                                            Length 236;
                                                                                                                                                                                                                       Query Match 44.4%; Score 36; DB 4; Length 236
Best Local Similarity 46.7%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.4%; Score 36;
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3558
LENGTH: 236
                                                                                                                                                              ; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                  4 KTPLTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                           65 KAPIQTLVALPVVEN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Staphylococcus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 EEYPLPTNAAAPV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 EKTPLTTAAXAPV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CRGANISM: Staphyloccocus
US-09-099-932-6
                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 28
US-09-446-301A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-446-301A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
TITLE: Proteolytic fragments and synthetic TITLE: peptides that block the binding of von Willebrand factor to the TITLE: platelet membrane glycoprotein 1b DOCUMENT NUMBER: EP 0 317 278 A2
  platelet glycoprotein Ib: A transmembrane protein with homology to leucine-rich alpha-2-glycoprotein Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB 1; Length blue. Pred. No. 3.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08119262B
Patent No. 5492809
CENERAL INFORMATION:
APPLICANT: Miller, Jonathan L.
APPLICANT: Cunningham, David
APPLICANT: Lyle, Vicki A.
APPLICANT: Finch, Clara N.
TITLE OF INVENTION: GLYCOPROTEIN ID ALPHA LESS REACTIVE
TITLE OF INVENTION: GLYCOPROTEIN ID ALPHA LESS REACTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATENTIN DATA:
APPLICATION NUMBER: US/08/119,262B
FILING DATE: 09-58P-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/821,717
FILING DATE: 15-JAN-1992
ATTOREY/AGBRY INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 16-NOV-1988
PUBLICATION DATE: 24-MAY-1989
RELEVANT RESIDUES IN SEQ ID NO: 6: FROM 0 TO 293
                                                                                                                                                           6: FROM 0 TO 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Nixon, Hargrave, Devans & Doyle STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20884/22
                                                                                                                                                           RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                 PUBLICATION INFORMATION:
AUTHORS: Zimmerman, Theodore S. AUTHORS: Ruggeri, Zaverio M. AUTHORS: Houghten, Richard A. AUTHORS: Vincete, Vincete AUTHORS: Mohri, Hiroshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Timain, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 201
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 42.9%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     409 EPTPIPTIATSPTI 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 610 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 EKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rochester : New York
     TITLE: plate
TITLE: to le
JOURNAL: Pro
VOLUME: 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 33
US-08-119-262B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: NCCOUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
TITLE OF INVENTION: POLYNUCLEOTIDES AND THEIR USE FOR DETECTING RESISTANCE TITLE OF INVENTION: TO STREPTOGRAMIN B AND RELATED TITLE OF INVENTION: COMPOUNDS FILE REFERENCE: 03715-0059
CURRENT PELLING DATE: 1999-12-20
NUMBER OF SEQ ID NOS: 51
SOFTWARE PARENT FILING DATE: 1999-12-20
SOFTWARE PARENT FILING DATE: 2.1
SOFTWARE PARENT FILING DATE: 2.1
SOFTWARE PARENT FILING DATE: 2.1
ENGTHARE PARENT FILING DATE: 3.1
                                                                                                                                                                                                                                                                                                                                                                     Length 507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Miller, Jonathan L.
APPLICANT: Cunningham, David
APPLICANT: Lyle, Vicki A.
APPLICANT: Lyle, Vicki A.
APPLICANT: Lyle, Vicki A.
TITLE OF INVENTION: MUTATIONS RENDERING PLATELET
TITLE OF INVENTION: GLYCOPROTEIN ID ALPHA LESS REACTIVE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/821,717B

FILING DATE: 15-JAN-1992

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Timain, Susan J.

REGISTATION NUMBER: 34,103

REFERENCE/DOCKET NUMBER: 20884/21

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPAX: (716) 263-1606

INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTENISTICS:

LENGTH: 610 amino acids

TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                  Query Match 44.4%; Score 36; DB 4; I
Best Local Similarity 61.5%; Pred. No. 2.7e+02;
Matches 8; Conservative 1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fujikawa, Kazuo

Hagen, Frederick S.

Papayannopoulou, Thalia

Cloning of the alpha chain of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/07821717B
Patent No. 5298239
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lopez, Jose A.
Chung, Dominic W.
                                                                                                                                                                                                                                                                                    ORGANISM: Staphylococcus sp
US-09-446-301A-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 EEYPLPTNAAAPV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 EKTPLTTAAXAPV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
PUBLICATION INFORMATION
AUTHORS: Lopez, Jose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-821-717B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS:
TITLE: C
                                                                                                                                                                                                                                                                  TYPE: PRT
```

g

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 610;
                                                                                                                                                                                                                                                                                                                           44.4%; Score 36; DB 1; Length 610; 42.9%; Pred. No. 3.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.4%; Score 36; DB 1; Length 610
42.9%; Pred. No. 3.3e+02;
tive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cuningham, David
APPLICANT: Lyle, Vicki A.
APPLICANT: Finch, Clara N.
APPLICANT: Finch, Clara N.
APPLICANT: Finch, Matthew R.
TITLE OF INVENTION: Mutations in the Gene Encoding the
TITLE OF INVENTION: Chain of Platelet Glycoprotein Ib
NUMBER OF SEQUENCES: 11
CORRESPONDENCES: 11
CORRESPONDENCES: Nixon, Hargrave, Devans & Doyle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: THE PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/234,265A
FILING DATE: 28-APR-1994
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Nixon, Hargrave, Devans & Doyle
Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
              REFERENCE/DOCKET NUMBER: 20884/23
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/08234265A Patent No. 5624817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34,103
34,103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 2
TELECOMMUNICATION INFORMATION
                                                                                                         TELEX: 978450
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 610 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (716) 263-1600
TELEX: 978450
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      409 EPTPIPTIATSPTI 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 EKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                          3 EKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 42.94
The Conservative
                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Miller,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Rochester
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-234-265A-11
                                                                                                                                                                                                                                                                                    US-08-135-929A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-234-265A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              factor to the
                                                                                                                                                                                                                                                           with homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                      PAGES: Dalling.

PAGES: Aug-1987

RELEVANT RESIDUES IN SEQ ID NO: 6: FROM 0 TO 610

PUBLICATION INFORMATION:
AUTHORS: Zimmerman, Theodore S.
AUTHORS: Suggesti, Zaverio M.
AUTHORS: Houghten, Richard A.
AUTHORS: Wincete, Vincete

AUTHORS: Mohri, Hiroshi

ITILE: Proteolytic fragments and synthetic peptides

ITILE: Proteolytic fragments and synthetic

ITILE: Proteolytic fragments

ITILE: Proteolytic fragments

ITILE: That block the binding of von Willebrand

ITILE: membrane glycoprotein Ib

TITLE: membrane glycoprotein Ib

TITLE: Last block the binding of von Willebrand

ITILE: membrane glycoprotein Ib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Mutations in the Gene Encoding the Alpha TITLE OF INVENTION: Chain of Platelet Glycoprotein Ib NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
       MOLECULE TYPE: protein
PUBLICATION INFORMATION:
AUTHORS: Lopez, Jose A.
AUTHORS: Chung, Dominic W.
AUTHORS: Hagen, Frederick S.
AUTHORS: Hagen, Frederick S.
AUTHORS: Roth, Garald J.
TITLE: Cloning of the alpha chain of human platelet
TITLE: glycoprotein Ib: A transmembrane protein
TITLE: leucine-rich alpha-2-glycoprotein
JOUNNEL: 84
PAGES: 5615-5619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36, DB 1; Length 610;
Pred. No. 3.3e+02;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: BATTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/135,929A
FILING DATE: 14-OCT-1993
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOCUMENT NUMBER: EP 0 317 278 A2
FILING DATE: 16-NOV-1988
PUBLICATION DATE: 24-MAY-1989
RELEVANT RESIDUES IN SEQ ID NO: 6: FROM 0 TO 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Nixon, Hargrave, Devans & Doyle STREET: Clinton Square, P.O. Box 1051 CITY: Rochester STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/08135929A
Patent No. 5593959
GENERAL INFORMATION:
APPLICANT: Miller, Jonathan L.
APPLICANT: Cunningham, David
APPLICANT: Lyle, Vicki A.
APPLICANT: Finch, Clara N.
APPLICANT: Pincus, Matthew R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 42.9%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ||: | | :| EPTPIPTIATSPTI 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 EKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 34
US-08-135-929A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-119-262B-6
```

δ

```
Sequence 26910, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
FALL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
                                                                                                                                                                                                                                                   TITLE OF INVENTION: No. 6348582el Prokaryotic Polynucleotides, TITLE OF INVENTION: Polypeptides and Their Uses NUMBER OF SEQUENCES: 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/936,165A
FILING DATE: 24-SEP-1997
CLASSIFICATION 536
PRIOR APPLICATION DATA:
APPLICATION NUBER: 60/027,032
FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35; DB 4;
Pred. No. 88;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                         SEE: SmithKline Beecham Corporation
: 709 Swedeland Road
King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                   Nicholas, Richard
Pratt, Julie
Reichard, Richard
                                                                                                                                                                                                                Rosenberg, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : ||: : |: |
106 DNTPINNSVNTPIITN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.2%;
25.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 EKTPLTTAAXAPVVXN 18
                                                                                                         Knowles, David
Lonetto, Michael
                                                                      Burnham, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 136 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Gimmi, Edward R
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                        Ward, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: Protein
                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                       Hodgson,
                                                                                                         Knowles,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-252-991A-26910
      Patent No. 6348582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-936-165A-461
                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                           PA
                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: CRABB, Brendan S.

APPLICANT: FENG, Li

TITLE OF INVENTION: EQUINE RHINOVIRUS I PROTEINS
FILE REFERENCE: 040268/0151
CURRENT PILING DATE: 2000-09-12
PRIOR PILING DATE: 2000-09-12
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-05
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-05
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-05
PRIOR FILING DATE: EARLIER FILING DATE: 1995-12-18
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTING DATE: 2000-09-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.4%; Score 36; DB 3; Length 2318; 53.3%; Pred. No. 1.5e+03; Live 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.4%; Score 36; DB 4; Length 2318; 53.3%; Pred. No. 1.5e+03; Live 1; Mismatches 6; Indels
                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: STUDDERT, Michael J.
APPLICANT: STUDDERT, Michael J.
APPLICANT: ERBB, Brendan S.
APPLICANT: ERBB, Li
TITLE OF INVENTION: EQUINE RHINOVIRUS 1 PROTEINS
FILE REFERENCE: 040268/0151;
CURRENT APPLICATION NUMBER: US/09/091,219
CURRENT FILING DATE: 1998-10-05
BARLIER APPLICATION NUMBER: PCT/AU96/00815
BARLIER PILING DATE: 1996-12-18
BARLIER FILING DATE: 1995-12-18
BARLIER FILING DATE: 1995-12-18
MUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Foot-and-mouth disease virus US-09-660-541-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Foot-and-mouth disease virus
US-09-091-219-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 38
US-08-936-165A-461
; Sequence 461, Application US/08936165A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 24, Application US/09660541
Patent No. 6531136
GENERAL INFORMATION:
APPLICANT: STUDDERT, Michael J.
                                                                                                                        Sequence 24, Application US/09091219
Patent No. 6171592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1609 ERQKPLKVKAKAPVV 1623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1609 EROKPLKVKAKAPVV 1623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 EEKTPLTTAAXAPVV 16
| ||: | : | : 409 EPTPIPTIATSPT1 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 53.3.
Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 24
LENGTH: 2318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-660-541-24
                                                                                   RESULT 36
US-09-091-219-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
```

Gaps

```
RESULT 40

US-00-252-91A-13221

Sequence 3221, Application US/09252991A

Petent No. 6551795

GENERAL INFORMATION:

APPLICATION:

APPLICATION:

TITLE OF INVENTION:

TOTAL APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 32221

LENGTH: 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                  Query Match

43.2%; Score 35; DB 4; Length 181;
Best Local Similarity 46.2%; Pred. No. 1.2e+02;
Matches 6; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35; DB 4; Length 185
Pred. No. 1.3e+02;
1; Mismatches 2; Indels
PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 26910 LENGTH: 181
                                                                                                                         TYPE: PRT (CRGANISM: Pseudomonas aeruginosa US-09-252-991A-26910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT;
CRCANISM: Pseudomonas aeruginosa
US-09-252-991A-32221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 43.2%;
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                   86 ERRSPATNSAAAP 98
                                                                                                                                                                                                                                                                                                                       2 EEKTPLTTAAXAP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S TPLTTAAXAP 14
                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
```

Search completed: January 28, 2004, 13:10:29 Job time : 22 secs

||| :|| || 9 TPLRSAATAP 18

g

Ч

```
Query Match
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
Sequence 1130, Ap
Sequence 10589, A
Sequence 22, Appl
Sequence 198, App
Sequence 198, App
Sequence 11701, A
Sequence 11701, A
Sequence 11701, A
                                                                                                                                                         January 28, 2004, 13:08:14; Search time 33 Seconds (without alignments) 119.030 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        '(gnz_6/ptodata/2/pubpaa/USO7_PUBCOMB.ppp:*
'(gnz_6/ptodata/2/pubpaa/USO7_NEW_PUB.ppp:*
'(gnz_6/ptodata/2/pubpaa/USO6_NEW_PUB.ppp:*
'(gnz_6/ptodata/2/pubpaa/USO6_NEW_PUB.ppp:*
'(gnz_6/ptodata/2/pubpaa/USO6_PUBCOMB.ppp:*
'(gnz_6/ptodata/2/pubpaa/USO8_NEW_PUB.ppp:*
'(gnz_6/ptodata/2/pubpaa/USO8_NEW_PUB.ppp:*
'(gnz_6/ptodata/2/pubpaa/USO8_PUBCOMB.ppp:*
'(gnz_6/ptodata/2/pubpaa/USO8_NEW_PUB.ppp:*
'(gnz_6/ptodata/2/pubpaa/USO8_NEW_PUB.ppp:*
'(gnz_6/ptodata/2/pubpaa/USO8_NEW_PUB.ppp:*
'(gnz_6/ptodata/2/pubpaa/USO9_PUBCOMB.ppp:*
'(gnz_6/ptodata/2/pubpaa/USO9_PUBCOMB.ppp:*
'(gnz_6/ptodata/2/pubpaa/USO9_PUBCOMB.ppp:*
'(gnz_6/ptodata/2/pubpaa/USO08_PUBCOMB.ppp:*
'(gnz_6/ptodata/2/pubpaa/USO08_PUBCOMB.ppp:*
'(gnz_6/ptodata/2/pubpaa/USO08_PUBCOMB.ppp:*
'(gnz_6/ptodata/2/pubpaa/USO08_PUBCOMB.ppp:*
'(gnz_6/ptodata/2/pubpaa/USO08_PUBCOMB.ppp:*
'(gnz_6/ptodata/2/pubpaa/USO08_PUBCOMB.ppp:*
'(gnz_6/ptodata/2/pubpaa/USO08_PUBCOMB.ppp:*
'(gnz_6/ptodata/2/pubpaa/USO08_PUBCOMB.ppp:*
'(gnz_6/ptodata/2/pubpaa/USO08_PUBCOMB.ppp:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 US-10-369-493-13806
2 US-10-136-705-1139
5 US-10-156-761-10589
4 US-10-078-929-198
5 US-10-156-761-13589
0 US-09-815-240-11701
0 US-09-815-240-11701
0 US-09-816-149-59
1 US-09-816-149-59
1 US-09-816-149-59
2 US-10-326-090-59
5 US-10-166-087-4
0 US-09-952-442A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                777136 segs, 206736638 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published Applications AA:*
                                                                                                                 - protein search, using sw model
                                                                                                                                                                                                                                                                                                         1 XEEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                            US-09-359-426C-2
81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1132
1132
1132
1132
1446
1446
1449
1449
1449
1155
1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      555.6

540.0

540.0

550.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

560.0

56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6:
77:
110:
111:
114:
115:
116:
                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB
Maximum DB
                                                                                                              OM protein
                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database
                                                                                                                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Result
```

```
Sequence 36, Appl
Sequence 92, Appl
Sequence 2209, Ap
Sequence 214, App
Sequence 214, App
Sequence 13813, A
Sequence 4429, Ap
Sequence 7187, App
Sequence 7187, App
                                                                                 Sequence 8852, Ap
Sequence 16863, A
Sequence 10971, A
Sequence 5890, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                              3, Appli
13, Appl
19305, A
20, Appl
8054, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3511, Ap
8511, Ap
1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
0 US-09-738-626-5663

0 US-09-952-422A-19

0 US-09-952-422A-19

0 US-09-952-423A-19

0 US-09-952-432-16863

2 US-10-369-439-16863

10S-109-156-761-10971

10S-09-768-866-562-95

0 US-09-764-846-214

5 US-10-032-585-7767

0 US-09-764-846-214

5 US-10-031-483-214

5 US-10-369-493-13813

2 US-10-369-493-13813

2 US-10-369-493-13813

2 US-10-369-493-1387

2 US-10-369-493-1387

2 US-10-369-493-1387

2 US-10-369-493-1387

2 US-10-369-493-187

2 US-10-369-493-1805

0 US-09-323-998D-57

0 US-09-323-998D-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-080-334-129
US-10-156-761-13000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
        233
395
395
395
507
1353
2280
2280
2277
277
277
478
495
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
19695
1969
                                                          US-10-369-493-13806
```

```
Sequence 13806, Application US/10369493

Sequence 13806, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Barry S.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

FILE REFERENCE: 38-10(52052)B

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR SEQ ID NOS: 47374

SEQ ID NO 13806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COTATION: (1). (478)
CTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Pseudomonas fluorescens
```

ö

Gaps

.. O

Indels

5

0; Mismatches

LTTAAXAPVVXN 18

RESULT

Sequence Sequence Sequence

Sequence

셤 ò

Score 45; Pred. No.

55.6%;

DB 12; Length 478; 17;

```
TITLE OF INVENTION:

ITLE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Weng, Zude
TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
TITLE OF INVENTION: Stress Response
FILE REPERENCE: BB1357 US NA
CURRENT APPLICATION NUMBER: US/10/078,929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB 14; Length 132;
Pred. No. 19;
1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 198, Application US/10078929
Publication No. US20020152497A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/566,394
PRIOR FILING DATE: 2000-05-05
PRIOR PELICATION NUMBER: 60/133038
PRIOR FILING DATE: 1999-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2000-05-05
APPLICATION NUMBER: 60/133038
APPLICATION NUMBER: 60/133042
APPLICATION NUMBER: 60/133042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60/133427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97 EAAPPTTTAAEAPAIAAA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Miao, Guo-Hua
Falco, Saverio Carl
Sakai, Hajime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Famodu, Omolayo O.
Odell, Joan T.
Meyers, Blake
Thorpe, Catherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.6%;
                            Omolayo 0.
                                                                                      Meyers, Blake
Thorpe, Catherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-078-929-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-078-929-198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Mic.
SEQ ID NO 22
LENGTH: 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                   TITLE OF INVENTION: POlynucleotides which are of nature B2/D+ A- and which are isolat TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolat TITLE OF INVENTION: E.coli, and biological uses of these polynucleotides and of their FILE OF INVENTION: E.COLI, and biological uses of these polynucleotides and of their CURRENT APPLICATION NUMBER: US/10/238,075
CURRENT FILING DATE: 2002-09-10
RIOR APPLICATION NUMBER: 0003145
RIOR APPLICATION NUMBER: 0003145
NUMBER OF SEQ ID NOS: 1576
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.3%; Score 44; DB 12; Length 306; 47.1%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 15; Length 483; 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 43; DB 1
Pred. No. 37;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: ARAKIY, WOSHIYUKI
APPLICANT: HATYORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR PLICATION DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10589, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
US-10-238-075-1139
. Sequence 1139, Application US/10238075
; Publication No. US20030148324A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22, Application US/10078929
Publication No. US20020152497A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: Streptomyces avermitilis US-10-156-761-10589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 EKVPCTSSGVAPIFVNA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 EKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rafalski, Antoni
APPLICANT: Miao, Guo-Hua
APPLICANT: Falco, Saverio Carl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Escherichia coli
US-10-238-075-1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 10589
LENGTH: 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 PLTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 54.3
Best Local Similarity 47.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLTTEAGAPVADN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 53.1
Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-156-761-10589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-078-929-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

```
APPLICANT: EDESTIE, JOSES
APPLICANT: EDESTIE, JOSES
APPLICANT: Knapp, Stefan
APPLICANT: Knapp, Stefan
APPLICANT: Hauser, Hans-Peter
TITLE OF INVENTION: RETROYIRUS FROM HIV GROUP AND ITS USE
FILE REFERENCE: 05495.0001-04
CURRENT APPLICATION NUMBER: US/09/886,156
CURRENT FILING DATE: 2001-06-22
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-10-06
PRIOR FILING DATE: 1992-10-06
PRIOR FILING DATE: 1992-10-06
PRIOR FILING DATE: 1992-10-06
PRIOR FILING DATE: 1992-10-07
PRIOR FILING DATE: 1992-10-07
PRIOR FILING DATE: 1992-10-07
PRIOR FILING DATE: 1992-10-07
PRIOR FILING DATE: 1993-06-01
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PATCHTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 10; Length 498;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
     APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB 9;
Pred. No. 1.1e+02;
                                                                                                       TITLE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR PAPLICATION NUMBER: 60/191,078
PRIOR PELLING DATE: 2000-03-21
PRIOR PELLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PELLING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-112-7
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-112-22
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR PILING DATE: 2001-12-26
PRIOR PILING DATE: 2001-12-26
PRIOR SEQ ID NOS: 14110
SOFTWARE: FARENSEE FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 59, Application US/09886156 Patent No. US20020155428A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.4%;
illarity 57.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    382 EQKTPLTAADMAAI 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Guertler, Lutz G.
APPLICANT: Eberle, Josef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 EEKTPLITAAXAPV 15
  Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-815-242-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 11701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-886-156-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-886-156-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49.4%; Score 40; DB 15; Length 346; 66.7%; Pred. No. 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 14; Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 1
Pred. No. 19;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, UUN
APPLICANT: HORIKAWA, HROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI MASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 15109
               PRIOR FILING DATE: 1999-05-11
PRIOR PEDLICATION NUMBER: 60/133428
PRIOR FILING DATE: 1999-05-11
PRIOR FILING DATE: 1999-06-11
PRIOR PLING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 208
SOFTWARE: Microsoft Office 97
SEQ ID NO 198
LENGTH: 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13589, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11701, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORWATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Streptomyces avermitilis US-10-156-761-13589
PRIOR APPLICATION NUMBER: 60/133437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 EAAPPTTTAAEAPAIAAA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.0%;
Matches 9; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 TPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 TVLTTAAAAAVVLSA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trawick, John D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 66.7
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                      TYPE: PRT

ORGANISM: Oryza sativa
US-10-078-929-198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-156-761-13589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-815-242-11701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
```

Gaps

; 0

Matches

a

ò

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BUELLE, UCBEL
APPLICANT: Brunn, Albrecht V.
APPLICANT: RAMPD, Stefan
APPLICANT: Hauser, Hans-Peter
TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE
FILE REFERENCE: 05495.0001-04
CURRENT FILING DATE: 1900-04
CURRENT FILING DATE: 1990-07-02
PRIOR APPLICATION NUMBER: US/09/109,916
PRIOR PILING DATE: 1992-10-06
PRIOR PILING DATE: 1992-10-06
PRIOR FILING DATE: 1992-10-06
PRIOR FILING DATE: 1992-10-22
PRIOR FILING DATE: 1992-10-30
PRIOR FILING DATE: 1992-10-30
PRIOR FILING DATE: 1992-10-20
PRIOR FILING DATE: 1992-10-20
PRIOR FILING DATE: 1992-10-30
PRIOR FILING DATE: 1993-06-01
                                                                                                                                                        49.4%; Score 40; DB 11; Length 498; 44.4%; Pred. No. 1.2e+02; ive 3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40; DB 11; Length 498;
Pred. No. 1.2e+02;
3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hauser, Hans-Peter
TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE
FILE REFERENCE: 05495,0001-04
CURRENT APPLICATION NUMBER: US/10/326,090
CURRENT FILING DATE: 2002-12-23
PRIOR APPLICATION UNBER: US/09/109,916
                                                                   ; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-886-149-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Human immunodeficiency virus US-09-886-159-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 59, Application US/10126090; Publication No. US20030166915A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               US-09-886-159-59
Sequence 59, Application US/0986159
Publication No. US20030003443A1
GENERAL INFORNATION:
APPLICANT: Guertler, Lutz G.
                                                                                                                                                                                                                                                                                      || :| |: |:| |:
119 EETSPRQTSQNYPIVTNA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 EETSPROTSONYPIVTNA 136
                                                                                                                                                                                                                                                            2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 44.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Guertler, Lutz G.
APPLICANT: Eberle, Josef
APPLICANT: Brunn, Albrecht V.
APPLICANT: Knapp, Stefan
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 59
LENGTH: 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eberle, Josef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 67
                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-326-090-59
                                                                                                                                                                                                              8;
                                                498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
    Gaps
       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                        APPLICANT: EDETIE, JOSEL
APPLICANT: Brunn, Albrecht V.
APPLICANT: Knapp, Stefan
APPLICANT: Hauser, Hans-Peter
TITLE OF INVENTON: RETROUNTING FROM HIV GROUP AND ITS USE
FILE REFERENCE: 05495.0001-04
CURRENT APPLICATION NUMBER: US/09/886,150
CURRENT PILING DATE: 2001-06-22
PRIOR FILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-06
PRIOR FILING DATE: 1992-10-06
PRIOR FILING DATE: 1992-10-06
PRIOR FILING DATE: 1992-10-30
PRIOR FILING DATE: 1992-10-32
PRIOR FILING DATE: 1992-10-30
PRIOR FILING DATE: 1993-10-22
PRIOR FILING DATE: 1993-10-22
PRIOR FILING DATE: 1993-10-30
PRIOR FILING DATE: 1993-10-30
PRIOR FILING DATE: 1993-06-01
NUMBER OF SEQ ID NOS: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 498;
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Eberle, Josef
APPLICANT: Brunn, Albrecht V.
APPLICANT: Knapp, Stefan
APPLICANT: Hanser, Hans-Peter
TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB 10; L
Pred. No. 1.2e+02;
3; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/886,149
CURRENT APPLICATION NUMBER: US/09/886,149
CURRENT FILING DATE: 2001-06-22
PRIOR PAPLICATION NUMBER: 09/109,916
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-10-06
PRIOR PILING DATE: 1992-10-06
PRIOR PILING DATE: 1992-10-06
PRIOR PILING DATE: 1992-10-06
PRIOR PILING DATE: 1992-10-22
PRIOR PILING DATE: 1992-10-22
PRIOR APPLICATION NUMBER: DE P 42 35 718.7
PRIOR PILING DATE: 1992-10-22
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P 43 18 186.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 59, Application US/09886149
Publication No. US20030003442A1
GENERAL INFORMATION:
                                                                                                                                                                                                                Sequence 59, Application US/09886150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ٠,
س
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 || :| |: |: |: || || EETSPRQTSQNYPIVTNA 136
                                                                                || :| |: |: || || 119 EETSPRQTSQNYPIVTNA 136
       ٠.
ښ
                                           2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 44.4%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1992-12-30
PRIOR APPLICATION NUMBER: DE FPRIOR FILING DATE: 1993-06-01
NUMBER OF SEQ ID NOS: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NOS: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Guertler, Lutz G.
                                                                                                                                                                                                                                    Patent No. US20020172939A1
GENERAL INFORMATION:
APPLICANT: Guertler, Lutz G.
       Conservative
                                                                                                                                                                                                                                                                                                               Eberle, Josef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Pate
SEQ ID NO 59
LENGTH: 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-886-149-59
         ..
80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-886-150-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT
```

ò

Gaps

. 0

Indels

Score 39; DB 10; Length 155; Pred. No. 50;

```
OTHER INFORMATION: Description of Artificial Sequence: Predicted AA OTHER INFORMATION: sequence of mouse SPAS-1
                                                                FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: SPAS-1 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.1%; Score 39; DB 10; Length 155; 66.7%; Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Shastri, Nilabh
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: SPAS.1 CANCER ANTIGEN
TITLE OF INVENTION: SPAS.1 CANCER ANTIGEN
FILE REFERENCE: 018941-001110US
CURRENT APPLICATION NUMBER: US/09/952,432A
CURRENT PILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: 60/234,472
PRIOR FILING DATE: 2000-09-21
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 16
LENGTH: 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5663, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 16, Application US/09952432A; Patent No. US2020150588A1; GENERAL INFORMATION: APPLICANT: Allison, James P. APPLICANT: Fasso, Marcella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIZOGUCHI, HIROSHI
ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                          48.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                                                                                                                                                                                Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Conservative
                                                                                                                                                                                                                                                     5 TPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 TPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                               :| |||| |||
60 SPTTTAATMPVV 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :| |||| ||||
60 SPTTTAATMPVV 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OZAKI
                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
US-09-952-432A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-952-432A-16
                                                                                                             US-09-952-432A-2
LENGTH: 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 16
                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/10166087
Sequence 4, Application US/10166087
Eublication No. US20030077767A1
GENERAL INFORMATION:
APPLICANT: Except Biosciences Inc.
APPLICANT: Staffa, Alfredo
APPLICANT: Zazopoulos, Emmanuel
APPLICANT: 3214-2US
CURRENT PERRENCE: 3014-2US
CURRENT FILING DATE: 2022-06-11
NUMBER OF SEQ ID NOS: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                     Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.4%; Score 40; DB 15; Length 500; 47.1%; Pred. No. 1.38+02; Live 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Streptomyces refuineus subspecies thermotolerans
US-10-166-087-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09952432A; Patent No. US20020150588A1; General INFORMATION:
GENERAL INFORMATION:
APPLICANT: Allison, James P.
APPLICANT: Shastri, Nilabh
APPLICANT: The Regents of the University of California; TITLE OF INVENTION: SPAS-1 CANCER ANTIGEN
TITLE OF INVENTION: SPAS-1 CANCER ANTIGEN
TITLE OF INVENTION SPAS-1 CANCER ANTIGEN
CURRENT APPLICATION NUMBER: US/09/952,432A; CURRENT EILING DATE: 2002-04-15
PRIOR FILING DATE: 2000-09-21
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                Query Match
49.4%; Score 40; DB 12; L
Best Local Similarity 44.4%; Pred. No. 1.2e+02;
Matches 8; Conservative 3; Mismatches 7;
              PRIOR FILING DATE: 1992-10-06
PRIOR APPLICATION NUMBER: DE P 42 35 718.7
PRIOR PILING DATE: 1992-10-22.
PRIOR APPLICATION NUMBER: DE P 42 44 541.8
PRIOR PILING DATE: 1992-12-30
PRIOR FILING DATE: 1992-12-30
PRIOR FILING DATE: 1993-06-01
NUMBER OF SEQ ID NOS: 67
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PATENTIN VEY: 2.0
PRIOR APPLICATION NUMBER: DE P 42 33 646.5
                                                                                                                                                                                                                                                                                           ) ORGANISM: Human immunodeficiency virus US-10-326-090-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        || :| |: |: || || 119 EETSPRQTSQNYPIVTNA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 EQTPLTTLRLAELIAEA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 EKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 47.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-952-432A-2
                                                                                                                                                                                                                           SEQ ID NO 59
LENGTH: 498
                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      а
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
```

ò

Gaps

ö

3; Indels

ø

```
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-369-493-16863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-369-493-16863
                                                                                                                                                                                                                                                                                                                                    US-10-369-493-8852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-369-493-8852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 8852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 395;
                                                                                                                                                                                                                         Score 39; DB 10; Length 233;
Pred. No. 79; 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Alliaon, James P.
APPLICANT: Fasco, Marcella
APPLICANT: Shastri, Nilabh
APPLICANT: Shastri, Nilabh
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: SPAS-1 CANCER ANTIGEN
FILE REFERENCE: 018941-001110US
CURRENT APPLICATION NUMBER: US/09/952,432A
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: 60/234,472
PRIOR PILING DATE: 2000-09-21
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21, Application US/09952432A
Patent No. US20020150588A1
GENERAL INFORMATION:
APPLICANT: Allison, James P.
APPLICANT: Fasso, Marcella
APPLICANT: Bastri, Milabh
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: SPAS-1 CANCER ANTIGEN
TITLE OF 108941-000110US
CURRENT APPLICATION NUMBER: US/09/952,432A
CURRENT FILING DATE: 2002-04-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ,4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.1%; Score 39; DB 10; 66.7%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 5663
LENGTH: 233
                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/234,472
PRIOR FILING DATE: 2000-09-21
NUMBER: OF SEQ ID NOS: 32
SOFTWARE: DEFINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19, Application US/09952432A Patent No. US20020150588A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Tumor SPAS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                  48.1%;
ilarity 66.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 SPTTTAATMPVV 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                   5 TPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                            || |:|: ||||
35 TPTTSASPAPVV 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 TPLTTAAXAPVV 16
                                                                                                                                                                                                                Query Match
Best Local Similarity
The B; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-952-432A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-952-432A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-952-432A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 19
LENGTH: 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                         임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
```

```
Sequence 16863, Application US/10369493
; Sequence 16863, Application US/10369493
; Publication No. US2003023367541
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Goldman, Warry S.
; APPLICANT: Goldman, Warry S.
; APPLICANT: Goldman, Warry S.
; APPLICANT: Goldman, Vianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: DAMYS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: DAMYS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION NUMBER: US/10/369,493
; CURRENT APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 16863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILLE OF INVENTION: EXPRESSION OF MICROBIAL PROFETIES
FILLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILLE OF INVENTION OF PLANTS WITH IMPROVED PROFETIES
FILLE OF INVENTION NUMBER: US/10/369, 493
FRIOR APPLICATION NUMBER: US 60/360, 039
FRIOR FILLING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                            ö
                                                                                                                                                            Gaps
                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 12; Length 477;
Pred. No. 1.8e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 12; Length 507;
                                                                                                    Score 39; DB 10; Length 395;
Pred. No. 1.4e+02;
L; Mismatches 3; Indels
FEATURE:
; OTHER INFORMATION: No. US20020150588A1mal SPAS-1'
US-09-952-432A-21
                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.1%; Score 39;
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8852, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Ralstonia metallidurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.1%;
                                                                                                         48.1%;
66.7%;
                                                                                Query Match
Best Local Similarity 66.7.
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 75.v.
Best Local 9, Conservative
                                                                                                                                                                                                                                                     300 SPTTTAATMPVV 311
                                                                                                                                                                                                                 5 TPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 LTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LTTAFGAPVVDN 12
```

```
CURRENT PELICATION NUMBER: US/10/353,690
CURRENT FILING DATE: 2003-01-29
PRIOR FILING DATE: 2003-01-29
PRIOR FILING DATE: 2002-02-01
PRIOR PELING DATE: 2002-03-15
PRIOR FILING DATE: 2002-03-15
PRIOR PILING DATE: 2002-04-19
PRIOR PELING DATE: 2002-04-19
PRIOR PELING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/376,287
PRIOR APPLICATION NUMBER: 60/376,287
PRIOR APPLICATION NUMBER: 60/376,287
PRIOR APPLICATION NUMBER: 60/390,971
PRIOR PELING DATE: 2002-06-24
PRIOR FILING DATE: 2002-06-24
PRIOR PELING DATE: 2002-07-03
PRIOR PELING DATE: 2002-07-03
PRIOR PELING DATE: 2002-07-10
PRIOR PELING DATE: 2002-08-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0

; LOCATION: (1)...(2080)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-353-690-36

                                                                                                                  US-10-353-690-36
; Sequence 36, Application US/10353690
; Publication No. US20030215840A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 OKTPLLSÁCIÁPLKOGA 151
                                                                                                                                                                                                                 APPLICANT: Logan, Thomas Joseph
APPLICANT: Chun, Miyoung
APPLICANT: Galvin, Katherine M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 EKTPLTTAAXAPVVXNA 19
||::|:| | ||:
EEESPASTQASTPVM 582
                                                                                                                                                                                                                                                                                                                                                                       Stagliano, Nancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 47.13
Matches 8; Conservative
                                                                                                                                                                                                                                                                                             Healy, Aileen
Acton, Susan L.
                                                                                                                                                                                                                                                                                                                                             Donoghue, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 2080
                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5890, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Geo, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Glaman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPERSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT FILING DATE: 2003-02-28
PRIOR PRILCATION NUMBER: US 6/360,039
PRIOR PRILCATION DATE: 2002-2221
                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
0
                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.1%; Score 39; DB 12; Length 1353; 46.7%; Pred. No. 5.7e+02; tive 4; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48.1%; Score 39; DB 15; Length 509; 52.9%; Pred. No. 1.9e+02;
47.1%; Pred. No. 1.9e+02; tive 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                            APPLICANI: INEDA, HARUO
APPLICANT: INEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 249-262
CURRENT FILING DATE: 2002-05-29
CURRENT FILING DATE: 2002-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 10971
LENGTH: 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                  Sequence 10971, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | ||||||| :: |
189 EITPLTTAALVDLLVEA 205
                                                                                                           185 EKTPLTALATQAILERA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 EKTPLTTAAXAPVVXNA 19
                                                                       3 EKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 46.79
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 5890
LENGTH: 1353
Best Local Similarity 47.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                   US-10-156-761-10971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-156-761-1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-369-493-5890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

```
TITLE OF INVENTION: Methods and compositions for treating
TITLE OF INVENTION: Methods and compositions for treating
TITLE OF INVENTION: cardiovascular disease using 1682, 6169, 6193, 7771, 14395
TITLE OF INVENTION: 29002, 33216, 43726, 69292, 26156, 32427, 2402, 7747, 1720
TITLE OF INVENTION: 14245, 58848, 1870, 25856, 32207, 1419, 1805, 16105, 38650, 1717LE OF INVENTION: 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912, 2868, TITLE OF INVENTION: 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914, 1771LE OF INVENTION: 51130, 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474, FILE REPERENCE: MPIO2-018PIRNOMIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.1%; Score 39; DB 12; Length 2080; 47.1%; Pred. No. 9.2e+02; Live 3; Mismatches 6; Indels
```

RESULT 24

2 EEKTPLTTAAXAPVV 16

```
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 27
US-09-764-846-214
                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THER
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                         APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Chaitenya S.
APPLICANT: Bangur, Chaitenya S.
APPLICANT: Bangur, Chaitenya S.
APPLICANT: Switzer, Anne
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER.
FILE REFERENCE: 210121.502
CURRENT APPLICATION NUMBER: US/09/866,562
CURRENT FILING DATE: 2011-05-25
NUMBER OF SEQ ID NOS: 96
SEQ ID NO 92
LENGTH: 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38; DB 10; Length 261;
Pred. No. 1.3e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                Score 38; DB 9; Length 229;
Pred. No. 1.2e+02;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 EKTPLKTTATPLSPLKPPRMDTAPVVAS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---XAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5209, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5209
Sequence 92, Application US/09866562
Patent No. US20020009758A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 39.3%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 5209
LENGTH: 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATEISHI, NAOKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SENOH, AKIHIRO
IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 PLTTAAXAPV 15
                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-866-562-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 EKTPLTTAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-738-626-5209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

|||||::|| 149 PLTTASASPV 158

g

RESULT 26

```
Sequence 7767,7,7
Sequence 7,7
Sequenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (6)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-846-214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 214, Application US/09764846

Patent No. US20020102688A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVERINCE: PTZ12

CURRENT APPLICATION NUMBER: US/09/764,846

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 348

SOFTWARE: Patentin Ver. 2.0

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38; DB 12; Length 276;
Pred. No. 1.4e+02;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin version 3.1
SEQ ID NO 7767
LENGTH: 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 KTPLTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 ETPLQTRAASPLTLN 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Candida albicans
US-10-032-585-7767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 46.7;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
```

.; 0

Length 478;

```
Publication No. US20030233675A1
Fublication No. US20030233675A1
GENERAL INFORMATION
APPLICANT: Goo, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: GOLDSON OF MICROBIAL PROPERTIES
FRIG APPLICATION NUMBER: US 60/360,039
PRICR APPLICATION NUMBER: US 60/360,039
PRICR APPLICATION NUMBER: US 60/360,039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4429, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Cao, Yongwei
APPLICANT: Gladmar, Barry S.
APPLICANT: Gradmar, Barry S.
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
46.9%; Score 38; DB 12; Length 49
Best Local Similarity 47.1%; Pred. No. 2.7e+02;
Matches 8; Conservative 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
FILE REPERENCE: 38-10(52052)B
CURRENT APPLICATION (52052)B
CURRENT PELLE REPERENCE: 2003-02-28
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-31
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 13813
TUDEL HIT 478
TUDEL HIT 478
                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB 12;
Pred. No. 2.6e+02;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas fluorescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burkholderia fungorum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 EKTPLTALAVNQILSEA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 EKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                             46.9%;
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 LTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |||||: ||| |
4 LTTASGAPVADN 15
                                                                                                                                                                                                                                                                                                                                                      US-10-369-493-13813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 31
US-10-369-493-7187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 30
US-10-369-493-4429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-369-493-4429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 4429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Stewen C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (254)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: misc feature LOCATION: (268)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (268)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc feature
LOCATION: (275)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (6) -
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (275)

VOHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: misc feature
LOCATION: (277)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                naturally occurring L-amino acids
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.9%; Score 38; DB 15; Length 277;
46.7%; Pred. No. 1.4e+02;
Live 3; Mismatches 5; Indels
                                           46.9%; Score 38; DB 10; Length 277;
46.7%; Pred. No. 1.4e+02;
ive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ12C1
CURRENT APPLICATION NUMBER: US/10/091,483
CURRENT FILING DATE: 2002-03-07
NUMBER OF SIG IO NOS: 348
Prior Application removed - See File Wrapper or Palm
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 214
LENGTH: 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Xaa equals any of the NAME/KEY: misc feature LOCATION: (254)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13813, Application US/10369493
Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                Sequence 214, Application US/10091483
Publication No. US20030049650A1
GENERAL INFORMATION:
                                                                                                                                                                                      ||: ||:||
120 TPVRPAAASPIVSGA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||: || :|:| |
120 TPVRPAASPIVSGA 134
                                                                                                                                                      5 TPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 TPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 46.73
Matches 7; Conservative
                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature LOCATION: (7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (261)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
                                                               Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 29
US-10-369-493-13813
                                                                                                                                                                                                                                                                                                                      US-10-091-483-214
                                              Query Match
                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                         ઠે
```

ô

Gaps

ö

Length 495;

ò

```
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: ELANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 6/360,039
PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Charanas, Stephane
APPLICANT: Cookson, William
APPLICANT: Moffat, Miriam
TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR NETHERTON'S DISEASE
FILE REFERENCE: 100317.70008.US
CURRENT APPLICATION NUMBER: US/10/220,510
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: GB 0005098.9
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VOR: 12.0
SEQ ID NO 13
; OTHER INFORMATION: Start codon: gga, Start position: nucleotide 1.
US-10-084-846A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: Peptide
                                                                                                      Length 19695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB 12; Length 19; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
                                                                                                                                                                                   3; Indels
                                                                                                             Score 38; DB 12;
Pred. No. 1.7e+04;
                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 19305, Application US/10369493; Publication No. US20030233675A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-220-510-13; Sequence 13, Application US/10220510; Publication No. US20030190637A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
                                                                                                             46.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Publication No. US20030190637A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                          15780 TPASTRAAAPVI 15791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 19305
                                                                                    Query Match
Best Local Similarity 58.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 EEKTPLTTAAXAP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 ESSTPGTTAASMP 15
                                                                                                                                                                                                                                                   5 TPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 35
US-10-369-493-19305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-220-510-13
                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22080, Application US/10369493
; Deblication No. US2003023675A1
; GENERAL INFORMATION:
   APPLICANT: Cao, Yongwei
   APPLICANT: Hinkle, Gregory J.
   APPLICANT: Steven C.
   APPLICANT: Stev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Protein 1: amino acid sequence encoded by coding strand 1.
                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 46.9%; Score 38; DB 12; Length 1679; Best Local Similarity 46.7%; Pred. No. 1.1e+03; Matches 7; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                                          DB 12; Length 495;
                                                                                                                                                                                                                                                          . 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3. Application US/10084846A
; Publication No. US2004006026A1
; GENERAL INFORMATION:
   APPLICANT: WEITHAUER, GABRIELE
; APPLICANT: WEITHAUER, GARES
APPLICANT: TREFZER, AKEL
APPLICANT: TREFZER, AKEL
APPLICANT: TREFZER, AKEL
APPLICANT: BEFINTON: AUGUSTON
TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
CURRENT APPLICATION NUMBER: US/10/084,846A
CURRENT PILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: PCT/EPO1/09815
PRIOR APPLICATION NUMBER: DE 101 09 166.4
PRIOR FILING DATE: 2001-02-25
NUMBER OF SEQ ID NOS: 120
SOFTWARE: PATCHIN VET: 3.2
                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Streptomyces viridochromogenes
                                                                                                                                                                                                                       Query Match 46.9%; Score 38; Best Local Similarity 47.1%; Pred. No. 3 Matches 8; Conservative 2; Mismatcl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Saccharomyces cerevisiae US-10-369-493-22080
                                                                                                                                                                                                                                                                                                                                                                                                                                174 EKTPLTALAVNQILSEA 190
                                                                                                                                                                                                                                                                                                                                                             3 EKTPLITAAXAPVVXNA 19
                                                                                    TYPE: PRT 'ORGANISM: Burkholderia cepacia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346 EEEATMTTSAVSPTV 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 EEKTPLITAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 32
US-10-369-493-22080
                                                                                                                                                           US-10-369-493-7187
                     SEQ ID NO 7187
LENGTH: 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-084-846A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                    ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
```

Gaps

0;

Length 480;

ò

g

```
Sequence 5.7, Application US/09323998D
Sequence 5.05020102631A1
GENERAL INFORMATION:
FAPELICANT: CUNNINGHAM JR., FRANCIS X.
APPLICANT: CUNNINGHAM JR., FRANCIS X.
TITLE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND METABOLISM AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPRENCE: 108172-09019
CURRENT APPLICATION NUMBER: US/09/323,998D
CURRENT APPLICATION NUMBER: US/09/323,998D
CURRENT APPLICATION NUMBER: 09/088,724
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 09/088,725
PRIOR APPLICATION NUMBER: 09/088,725
PRIOR PILING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-02
PRIOR PILING DATE: 1996-03-29
NUMBER OF SEQ ID NOS: 61
SEQ ID NO 57
SEQ ID NO 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SUN, ZAIREN
TITLE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND METABOLISM AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 108172-09019
CURRENT APPLICATION NUMBER: US/09/323,998D
CURRENT APPLICATION DATE: 1999-06-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 37; DB 10; Length 498; pred. No. 4.18+02; 0; Mismatches 3; Indels
                                                                                                                 Query Match
45.7%; Score 37; DB 12; Length 48
Best Local Similarity 47.1%; Pred. No. 3.9e+02;
Matches 8; Conservative 1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILLING DATE: 1959-00-02
PRIOR PLING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-02
PRIOR PELING DATE: 1998-06-02
PRIOR PILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 08/937,155
PRIOR PILING DATE: 1997-09-25
PRIOR PILING DATE: 1996-03-25
PRIOR PILING DATE: 1996-03-25
PRIOR PILING DATE: 1996-03-29
NUMBER: OF SEQ ID NOS: 61
SOFTWARE: PATCHIN VOY: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 58, Application US/09323998D Patent No. US20020102631A1 GENERAL INFORMATION: APPLICANT: CUNNINGHAM JR., FRANCIS X. APPLICANT: SUN, ZAIREN
                           ORGANISM: Rhodobacter sphaeroides
                                                                                                                                                                                                                                                                                             162 EKTPLTALASMAIFGRA 178
                                                                                                                                                                                                                                   3 EKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        370 TLAAAPVVANA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 TAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
CORGANISM: Capsicum sp.
US-09-323-998D-57
                                                          US-10-369-493-8054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-323-998D-58
                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-323-998D-57
   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Stewen C.
APPLICANT: Glodman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10 (52052) B
FULE REPERENCE: 38-10 (52052) B
FULE REPERENCE: 30-305-32-38
PRIOR FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20, Application US/09323998D

Patent No. US20020102631A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: CUNNINGHAM JR., FRANCIS X.

TITLE OF INVENTION: GENES OF CARCTENOID BIOSYNTHESIS AND METABOLISM AND TITLE OF INVENTION: METHODS OF USE THEREOF

FILE REFERENCE: 10972-09019

CURRENT FILING DATE: 1999-06-02

PRIOR APPLICATION NUMBER: US/09/323,998D

CURRENT FILING DATE: 1999-06-02

PRIOR FILING DATE: 1999-06-02

PRIOR FILING DATE: 1999-06-02

PRIOR APPLICATION NUMBER: 09/088,725

PRIOR APPLICATION NUMBER: 09/084,725

PRIOR APPLICATION NUMBER: 09/084,125

PRIOR FILING DATE: 1996-06-02

PRIOR PRILING DATE: 1996-06-02

SOFTWARE: PATENT ON UMBER: 08/524,125

RUMBER OF SEQ ID NOS: 61

SEQ ID NO 20

LENGTH 456
                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Consensus; OTHER INFORMATION: sequence of four plant B-cyclases US-09-323-998D-20
                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 45.7%; Score 37; DB 10; Length 456; Best Local Similarity 72.7%; Pred. No. 3.7e+02; Matches 8; Conservative 0; Mismatches 3; Indels
                                                                                                                    Length 445;
                                                                                                                 Query Match 45.7%; Score 37; DB 12; Length 44 Best Local Similarity 46.7%; Pred. No. 3.6e+02; Matches 7; Conservative 3; Mismatches 5; Indels
; LOCATION: (1). (445)
; OTHER INFORMATION: unsure at all Xaa locations US-10-369-493-19305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8054, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                      2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                          21 EEPTPIQAAALPPLL 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 8054
LENGTH: 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           336 TLAAAPVVANA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 TAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-369-493-8054
                                                                                                                                                                                                                                                                                                                                                                                                               US-09-323-998D-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
```

g

ò

ö

Gaps

```
ö
                                                                                                                                                                                                                                                                                                                                                                               RESULT 40

US-09-323-998D-59

i Sequence 59, Application US/09323998D

i Patent No. US20020102611A1

CENERAL INFORMATION:

APPLICANT: CUNNINGHAM JR., FRANCIS X.

APPLICANT: SUN, ZAIREN

TITLE OF INVENTION: METHODS OF CAROTENOID BIOSYNTHESIS AND METABOLISM AND

TITLE OF INVENTION: METHODS OF USE THEREOF

CURRENT FILING DATE: 1099-06-02

PRIOR PELLING DATE: 1998-06-02

PRIOR PELLOATION NUMBER: 09/088,724

PRIOR PELLOR DATE: 1998-06-02

PRIOR PELLING DATE: 1996-06-02

PRIOR PELLOR DATE: 1996-03-25

PRIOR PELLING DATE: 1996-03-25

TURBER OF SEQ ID NOS: 61

SOFTWARE: PAT

CORGANISM: Nicotiana SP.

US-09-323-998D-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0, Gaps
                                                                                                                              Score 37; DB 10; Length 500;
Pred. No. 4.1e+02;
0; Mismatches 3; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 10; Length 500;
Pred. No. 4.1e+02;
0; Mismatches 3; Indels
LENGTH: 500
TYPE: PRT
CRGANISW: Lycopersicon esculentum
US-09-323-998D-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative (
                                                                                                                                    Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                      372 TLAAAPVVANA 382
                                                                                                                                                                                                                                                    9 TAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                          g
```

Search completed: January 28, 2004, 13:11:14 Job time : 33 secs

9 TAAXAPVVXNA 19 | | | | | | | | 372 TLAAAPVVANA 382

상 원

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

January 28, 2004, 13:06:34; Search time 21 Seconds (without alignments) 87.010 Million cell updates/sec

US-09-359-426C-2 81 Title: Perfect score:

1 XEEKTPLTTAAXAPVVXNA 19 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | ď | | | SOUTHWINES | |
|--------|-------|-------|--------------|----|------------|--------------------|
| Result | | Ouery | | | | |
| No. | Score | Match | Match Length | DB | qı | Description |
| - | 63 | 77.8 | 482 | 7 | B83113 | catalase PA4236 [i |
| 2 | 53 | 65.4 | 484 | 7 | A58663 | catalase (EC 1.11. |
| e | 48 | 59.3 | 480 | 7 | AB0148 | catalase (EC 1.11. |
| 4 | 46 | 56.8 | 262 | 7 | T33408 | hypothetical prote |
| S | 46 | | 262 | 7 | E88400 | protein H34I24.2 [|
| 9 | 45 | 55.6 | 128 | 7 | JC1273 | ribosomal protein |
| 7 | 44 | 54.3 | 306 | 7 | AE0963 | probable carbohydr |
| ω | 44 | 54.3 | 427 | 7 | F85436 | hypothetical prote |
| 6 | 43 | 53.1 | 483 | 7 | S37055 | |
| 10 | 42 | 51.9 | 105 | 7 | A44639 | |
| 11 | 42 | 51.9 | 321 | 7 | T08462 | hypothetical prote |
| 12 | 42 | 51.9 | 436 | ~ | T46107 | hypothetical prote |
| . 13 | 41 | 9.05 | 132 | ~ | T50779 | aper |
| 14 | 41 | 50.6 | 482 | 7 | S60757 | catalase (EC 1.11. |
| 15 | 40 | 49.4 | | 7 | T31478 | hypothetical prote |
| 16 | 40 | 49.4 | 252 | 7 | H72469 | _ |
| 17 | 40 | 49.4 | 258 | 7 | AD1328 | |
| 18 | 40 | 49.4 | | 7 | E87611 | _ |
| 19 | 40 | 49.4 | | 7 | S05661 | υ |
| 20 | 40 | 49.4 | 1360 | 7 | T31674 | hypothetical prote |
| 21 | 39.5 | 48.8 | 405 | N | JQ2147 | OHP1 protein - mai |
| 22 | 39 | 48.1 | 486 | ~ | S10772 | 2-hydroxymuconic s |
| 23 | 39 | 48.1 | 507 | N | B87400 | aldehyde dehydroge |
| 24 | 39 | 48.1 | 527 | 7 | S46088 | |
| 25 | 39 | 48.1 | 1353 | 7 | T26301 | |
| 26 | | 47.5 | 1658 | 7 | D75489 | |
| 27 | 38 | 46.9 | 143 | 7 | S68226 | growth-blocking pe |
| 28 | 38 | 46.9 | 307 | 7 | T40089 | cytochrome c1, hem |
| 29 | 38 | 46.9 | 307 | ~ | A35125 | phospholipase D (E |

| hypothetical process | peptidase, M20/M25 | hypothetical prote | peptidase (M3 fami | hypothetical prote | probable translati | protein F58A4.11 [| hypothetical prote | probable secreted | probable phosphory | catalase (EC 1.11. | lycopene beta-cycl |
|----------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|
| 840750 | E87650 | S40983 | F81313 | T25603 | D71283 | F88561 | 848385 | G86194 | F72332 | C83492 | T01225 | T35518 | S72992 | T42038 | 872505 |
| 7 | N | ~ | N | 7 | ~ | 7 | N | ~ | ~ | 7 | 7 | 7 | ~ | 7 | 7 |
| 348 | 474 | 532 | 573 | 684 | 695 | 747 | 1679 | 200 | 71 | 116 | 328 | 347 | 463 | 488 | 200 |
| 46.9 | 46.9 | 46.9 | 46.9 | 46.9 | 46.9 | 46.9 | 46.9 | 46.3 | 45.7 | 45.7 | 45.7 | 45.7 | 45.7 | 45.7 | 45.7 |
| 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 37.5 | 37 | 37 | 37 | 37 | 37 | 37 | 37 |
| 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

catalase PA4236 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep_2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

M.J.; Br K.; Lim, C; Accession: B83113
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, I. S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000

A,Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathr A,Reference number: A82950; MUID:20437337; PMID:10984043

A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Molecule: 1-482 <STO>
A;Cross-treferences: GB:AE004841; GB:AE004091; NID:g9950451; PIDN:AAG07624.1; GSPDB:GN001
A;Experimental source: strain PAO1

C,Genetics: A,Gene: katA; PA4236 C,Superfamily: catalase

Gaps 0; 77.8%; Score 63; DB 2; Length 482; 82.4%; Pred. No. 0.0041; ive 0; Mismatches 3; Indels Query Match 77.8
Best Local Similarity 82.4
Matches 14; Conservative

ö

2 EEKTPLTTAAXAPVVXN g ò

18

18 2 EEKTRLTTAAGAPVVDN

catalase (EC 1.11.1.6) [validated] - Proteus mirabilis C,Species: Proteus mirabilis A,Variety: strain Pr, peroxide resistant C,Date: 19-Nov-1997 #sequence_revision 21-Nov-1997 #text_change 15-Sep-2000

C; Accession: A58663; B58663.
R; Buzy, A.; Bracchi, V.; Sterjiades, R.; Chroboczek, J.; Thibault, P.; Gagnon, J.; Jouve, B. Bracchi, V.; Sterjiades, R.; Chroboczek, J.; Thibault, P.; Gagnon, J.; Jouve, J. Protein Chem. 14, S9-72, 1998
A; Pritie: Complete amino acid sequence of Proteus mirabilis PR catalase. Occurrence of a A; Reference number: A58663; MUID:95305957; PMID:7786407
A; Accession: A58663
A; Accession: A58663
A; Accession: B58663
A; Accession: B58663
A; Accession: B58663
A; Accession: B58663
A; Residues: 1-305, As. aBuzz>
B; Gouet, P.; Jouve, H. M.; Dideberg, O. submitted to the Brookhaven Protein Data Bank, June 1996
A; Reference number: A67899; PDB:20AB
A; Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 3-475

```
C;Species Caenorhabditis elegans
C;Species Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: E88400
C;Accession: E88400
C;Accession: E88400
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolow A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolow A;Title: Genome sequence of the newatode C. elegans: a platform for investigating biolow A;Title: Genome sequence of the newatode C. elegans: a platform for investigating biolow A;Title: Genome sequence of the newatode C. elegans: a platform for investigating biolow A;Title: Genome sequence of the newatode C. elegans: a platform for investigating biolow A;Title: Genome sequence of the newatode C. elegans: a platform for investigating biolow A;Title: Genome sequence of the newatode C. elegans: a platform for investigating biolow A;Title: Genome sequence of the newatode C. elegans: a platform for investigating biolow A;Title: Genome sequence of the newatode C. elegans: a platform for investigating biolow A;Title: Genome sequence of the newatode C. elegans: a platform for investigating biolow A;Title: Genome sequence of the newatode C. elegans: a platform for investigating biolow A;Title: Genome sequence of the newatode C. elegans: a platform for investigating biolow A;Title: Genome sequence of the newatode C. elegans: a platform for investigating biolow A;Title: Genome sequence of the newatode C. elegans: a platform for investigating biological A;Title: Genome sequence of the newatode C. elegans: a platform for investigating biological A;Title: Genome sequence of the newatode C. elegans: a platform for investigating biological A;Title: Genome sequence of the newatode C. elegans: a platform for investigating biological A;Title: Genome sequence of the newatode C. elegans: a platform for investigating biological A;Title: Genome sequence of the newatode C. elegans: a platform for investigation for investigation for 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ribosomal protein L7/L12 - Streptomyces antibioticus
C;Species: Streptomyces antibioticus
C;Species: Streptomyces antibioticus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C;Accession: JC1273
R;Parra, F.; Blanco, G.; Alonso, J.M.M.; Balbin, M.; Mendez, C.; Salas, J.A.
A;Title: Cloning and sequence of a gene encoding the L7/L12 ribosomal protein equivalen.
A;Reference number: JC1273; MUID:92380478; PMID:1511874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-262 <STO>
A;Cross-references: GB:chr_III; PIDN:AAC26925.1; PID:g3329614; GSPDB:GN00021; CESP:H34L
                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-262 <LAT>
A;Cross-references: EMBL:AF078784; PIDN:AAC26925.1; GSPDB:GN00021; CESP:H34124.2
A;Experimental source: strain Bristol N2; clone H34124
                        C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C;Accession: T33408 R;Latrellle, P.; Wamsley, P.; O'Brien, D. R;Latrellle, P.; Wamsley, P.; O'Brien, D. A;Description: The sequence of C. elegans cosmid H34124.

A;Reference number: 221340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Residues: 1-128 <PAR>
A, Residues: 1-128 <PAR>
A, Cross-references: GB-M89911, NID:g153436, PIDN:AAA26811.1; PID:g153438
C;Superfamily: Bscherichia coli ribosomal protein Li2
C;Keywords: protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 262,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Note: intron positions not resolved (incomplete sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein H34I24.2 [imported] - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 46; DB 2;
Pred. No. 1.9;
3; Mismatches
                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; tränslated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46; DB 2;
Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||||||| : | |: ||
190 KTPLTSGSSARVINNA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||||: : | |: ||
190 KTPLTSGSSARVINNA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 KTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 KTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.8%;
C;Species: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 56.8
Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: CESP: H34I24.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Molecule type: DNA
                                                                                                                                                                                                                                                                      A;Accession: T33408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: JC1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: H34I24.2
A;Map position: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ۍ
د.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Crystal structure of Proteus mirabilis PR catalase with and without bound NADPH A; Reference number: A58664; MUID:95311317; PMID:7791219
A; Reference number: A58664; MUID:95311317; PMID:7791219
A; Contents: annotation; X-ray crystallography, 2.2 angstroms
C; Complex: homotetramer
C; Complex: homotetramer
C; Function:
C; Function: catalyzes the conversion of two of molecules of hydrogen peroxide to two A; Note: this enzyme has a tightly bound NADPH cofactor
C; Superfamily: catalase
C; Keywords: chromoprotein; heme; homotetramer; iron; metalloprotein; NADP; oxidoreductas
C; Keywords: chromoprotein; heme sulfone (Met) #status experimental
F; 54, 93, 127/Active site: His, Ser, Ash #status predicted
F; 54, 83, 127/Active site: His, Ser, Ash #status predicted
F; 337/Binding site: heme iron (Tyr) (axial ligand) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: AB0148
R; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. Geno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-480 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC90045.1; PID:g15979266; GSPDB:GN00175
                                                                                                                                                                                        Signoue, P.; Jouve, H.M.; Hajdu, J.

submitted to the Brookhaven Protein Data Bank, June 1996

A.Reference number: A67901; PDB:2CAG

A.Reference number: A67901; PDB:2CAG

A.Contents: annotation; X-ray crystallography, 2.7 angstroms, residues 3-475

A.Note: compound II, dithiothreitol reduced compound I

R.Gouet, P.; Jouve, H.M.; Dideberg, O.

Submitted to the Brookhaven Protein Data Bank, July 1996

A.Reference number: A67902; PDB:2CAH

A.Contents: annotation; X-ray crystallography, 2.7 angstroms, residues 3-475
    R;Gouet, P.; Jouve, H.M:; Hajdu, J.
submitted to the Brookhaven Protein Data Bank, June 1996
A;Reference number: A67900; PDB:2CAF
A;Reference annotation; X-ray crystallography, 2.7 angstroms, residues 3-475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A,Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein H34I24.2 - Caenorhabditis elegans (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          catalase (EC 1.11.1.6) [imported] - Yersinia pestis (strain CO92)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 65.4%; Score 53; DB 2; Similarity 75.0%; Pred. No. 0.22; 12; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2
1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Note: native Fe(III) with NADPH
R;Gouet, P.; Jouve, H.M.; Dideberg, O.
J. Mol. Biol. 249, 933-954, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ٦,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKKGLTTAAGAPVVDN 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 EKTPLTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 EKTPLTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
A;Gene: katA
C;Superfamily: catalase
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: AB0148
A; Status: preliminary
                                                                                                                                                                    A;Note: compound I
R;Gouet, P.; Jouve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
```

8

ö

Best Loc

ઠે 셤 RESULT 4

g

8

```
C;Accession: T08462

*Xouerier: F.; Purnelle, B.; Boutry, M.; Goffeau, A.; Salanoubat, M.; Mewes, H.W.; Mayersubmitted to the Protein Sequence Database, May 1999

A;Reference number: 216420
                    C;Date: 10-Dec-1993 #sequence_revision 26-May-1995 #text_change 04-Mar-2000 C;Accession: S37055 R;Reacy, S.; van Pee, K.H.; Vining, L.C. R;Reacy, S.; van EMBL Data Library, August 1993 A;Reference number: S37055 A;Accession: S37055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein F2206.250 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Streptomyces coelicolor
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 31-Oct-1997
                                                                                                                                                                                                                                                                                                                                  PIDN:CAA52796.1; PID:9581780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Ke_words: chromoprotein; heme; iron; metalloprotein; oxidoreductase F;54,93,127/Active site: His, Ser, Asn #status predicted F;337/Binding site: heme iron (Tyr) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: T08462
A;Molecule type: DNA
A;Kesidues: 1-321 <QUE>
A;Cross--references: EMBL:AL050300; GSPDB:GN00061; ATSP:F2206.250
A;Experimental source: cultivar Columbia; BAC clone F2206
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         catalase (EC 1.11.1.6) - Streptomyces coelicolor (fragments)
                                                                                                                                                                                                                                                                                        A;Residues: 1-483 <FAC>
A;Cross-references: EMBL:X74791; NID:g397888; PIDN:CAA52796
A;Note: the source is designated as Streptomyces venezuelae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Walker, G.
submitted to the Protein Sequence Database, September 1994
A;Reference number: A44639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 42; DB 2;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 43; DB 2;
Pred. No. 12;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42; DB;
Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.9%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.9%;
Streptomyces violaceus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 53.1%;
Best Local Similarity 69.2%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 PLTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 PLTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 PLTTEAGAPVADN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 PLTTVAGAPVPDN 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: catalase
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein A; Residues: 1-105 < WAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Superfamily: catalase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: ATSP: F2206.250
A; Map position: 3
                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: A44639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A44639
                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                       Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T08462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A44639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                probable carbohydrate kinase STV3989 [imported] - Salmonella enterica subsp. enterica se CS-species: Salmonella enterica subsp. enterica serovar Typhi A,Note: this species has also been called Salmonella typhi C;Bote: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cyaces of Secondary Agogenesis of Secondary Accession: Agogenesis of Secondary Secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rianonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
Nature 402, 769-777, 1991
A;Title: Sequence and analysis of Chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-427 <STO>
A;Cross-references: GB:NC_001268; NID:g7270646; PIDN:CAB80363.1; GSPDB:GN00140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein AT4g36970 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 427;
                               DB 2; Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Length 306;
                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             catalase (EC 1.11.1.6) alpha-2 chain - Streptomyces violaceus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44; DB:
Pred. No. 4.9;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44;
Pred. No.
                                  Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | | | | | :: | | |: | | | EKVPCTSSGVAPIFVNA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 EKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.3%;
                               Query Match
Best Local Similarity 66.7%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||| :||| :|||
208 EEKAEMTTAMQSPVV 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 54.3%;
Best Local Similarity 47.1%;
Matches 8; Conservative
                                                                                                                                                           2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                          EEKFDVTAAAAAPVV 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 60.0°
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: F85436
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: F85436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: AT4g36970
A; Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
S37055
```

g

ઠે

g

ò

ö

```
C; Accession: H72469

C; Accession: H72469

S; Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takal awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; DNA Res. 6, 83-101, 1999

A; Hille: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy. A; Reference number: A72450; MUID:99310339; PMID:10382966

A; Accession: H72469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: DDBJ:AP000064; NID:g5105945; PIDN:BAA81416.1; PID:d1045202; PID:g510825. B; A;Gene: APE2401
                         A,Molecule type: DNA
A,Rosidues: 1-482 <DES>
A,Cross-references: EMBL:U07800; NID:g494943; PIDN:AAA18481.1; PID:g494944
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1994
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-171 (MTL)
A;Cross-references: EMBL:Z82273; PIDN:CAB54978.1; GSPDB:GN00022; CESP:F56F12.1
A;Experimental source: clone F56F12
C;Genetics:
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T31478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein APE2401 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                              A/Gene: catA
C,Superfamily: catalase
C,Superfamily: catalase
C,Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F;57,96,130/Active site: His, Ser, Asn #status predicted
F;340/Binding site: heme iron (Tyr) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 252;
                                                                                                                                                                                                                                                                                                 Length 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F56F12.1 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB 2;
Pred. No. 13;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB 2;
Pred. No. 20;
0; Mismatches
                                                                                                                                                                                                                                                                                            Score 41; DB 2;
Pred. No. 27;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: Z21039
A;Acterence number: Z21039
A;Acterence number: Z21039
A;Acterence number: Z21039
                                                                                                                                                                                                                                                                                                    50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 53.3%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 TPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 TPTTTTAAAPIAAVA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                           Best Local Similarity 75.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    7 LTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-252 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: CESP: F56F12.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 4
A; Introns: 16/2; 50/1
                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C,Accession: S60757
R,DeShazer, D.; Wood, G.E.; Friedman, R.L.
Mol. Microbiol. 14, 123-130, 1994
A,Title: Molecular characterization of catalase from Bordetella pertussis: identificatio A;Reference number: S60757; MUID:95131725; PMID:7830550
A,Accession: S60757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: T50779
R;Himelblau, E.; Mira, H.; Lin, S.J.; Culotta, V.C.; Penarrubia, L.; Amasino, R.M.
Bjant Physiol. 11, 1227-1234, 1998
A;Title: Physiol. 11, 1227-1234, 1998
A;Title: Monthification of a functional homolog of the yeast copper homeostasis gene ATX
A;Reference number: 224450; MUID:9701579; PMID:9701579
                                                                                                                                                                                                                                                                                                                                X.
                                                                                                                                                                                                                                                 Cipecies: Arabidopsis thaliana (mouse-ear cress)
CiDate: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
CiDate: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
CiAccession: T46107
Rialcaraz, J.P.; Clabault, G.; Cottet, A.; Mache, R.; Mewes, H.W.; Lemcke, K.; Mayer, Submitted to the Protein Sequence Database, January 2000
A;Reference number: 223021
A;Reference number: 223021
A;Recession: T46107
A;Accession: T46107
A;Accession: T46107
A;Residues: L436 ALC
A;Cross-references: EMBL:All32972
A;Experimental source: cultivar Columbia; BAC clone T25B15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         catalase (EC 1.11.1.6) - Bordetella pertussis
C;Species: Bordetella pertussis
C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Oryza sativa (rice)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Dec-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
       Gaps
          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                  hypothetical protein T25B15.140 - Arabidopsis thaliana
            .,
60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
A;Residues: 1-132 - 4HIM>
A;Cross-references: EMBL:AF198626; PIDN:AAF15285.1
C;Superfamily: copper homeostasis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  copper chaperone homolog CCH [imported] - rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.6%; Score 41; 50.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                          291 EEKTPVEKKTGVPVVKKA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEKTPVEKKTGVPVVKKA 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EAAPPTTTÄÄEÄPAIAAÄ 114
            1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 EEKTPLTTAAXAPVVXNA 19
                                                       2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 51.9%;
Best Local Similarity 50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C,Genetics:
A,Map position: 3
A,Introns: 418/1
A,Note: T25815.140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: T50779
            .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
                                                                                                                                                                                    RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
                                                            ઠે
                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Į
```

ö

```
L.M.; Fr
                                                                            a Drosophila muscari
                                                                                                                                                                                                                                    A,Cross-references: EMBL:M23412; NID:g157829; PID:g157830
R;Shapiro, R.A.; Wakimoto, B.T.; Subers, E.M.; Nathanson, N.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 9039-9043, 1989
A;Title: Characterization and functional expression in mammalian cells of genomic and cl. A;Reference number: A36191; MUID:90046926; PMID:2510174
                                                                                                                                                                                                                                                                                                                                                                                                                    A:Molecule type: mRNA
A:Molecule type: mRNA
A;Residues: 81-154, T',156-198,'N',200-215,'G',217-227,229-330,'P',332-426,'YATPVTIETPL
A;Cross-references: GB:M27495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neurotransmitter receptor; transm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein 1 - fruit fly (Drosophila simulans) retrotransposon ninja (fragmen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ninja in Drosophila simulans.
R;Onai, T.; FitzGerald, M.G.; Arakawa, S.; Gocayne, J.D.; Urquhart, D.A.; Hall, FEBS Lett. 255, 219-225, 1989
A;Title: Cloning, sequence analysis and chromosome localization of a Drosophila A;Reference number: S05661; MUID:90005981; PMID:2507354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-1360 <OGU>
A; Cross-references: EMBL:D83207; NID:d1068446; PID:d1020552; PIDN:BAA19771.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J02147
OHP1 protein - maize
C;Species: Zea mays (maize)
C;Date: 28-Mug-1985 #sequence_revision 07-Oct-1994 #text_change 26-May-2000
C;Accession: J02147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Drosophila simulans
C;Species: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: T31674
R; Ogura, K; Takechi, S.; Nakayama, T.; Yamamoto, M. Genes Genet. Syst. 71, 1-8, 1996
A; Title: Molecular structure of the transposable element A; Reference number: Z21057; MUID:96252483; PMID:8925473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.4%; Score 40; DB 2; Le 47.1%; Pred. No. 1.3e+02; cive 2; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40; DB 2;
Pred. No. 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: T31674
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;20-243/Domain: transmembrane #status predicted
F;268-289/Domain: transmembrane #status predicted
F;702-722/Domain: transmembrane #status predicted
F;739-758/Domain: transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #status predicted #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: FlyBase:FBgn0015168
A;Mobile element: retrotransposon ninja
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Cross-references: FlyBase: FBgn0000037
A, Map position: 2R 60C5-C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Keywords: G protein-coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Experimental source: strain Oregon C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | | |||| ||:
| 602 EDGPTTTAAAAPLASAA 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 EATPITTASQQPASSGA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 47.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;104-127/Domain: transmembrane
F;141-161/Domain: transmembrane
F;179-200/Domain: transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 EKTPLTTAAXAPVVXNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 EKTPLTTAAXAPVVXNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: FlyBase: mAcR-60C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 9; Conserv
                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-788 < ONA>
                                                                                                                                             A; Accession: S05661
                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A36191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                              hypothetical protein Imc2028 [imported] - Listeria monocytogenes (strain EGD-e) C;Species: Listeria monocytogenes (Jate: 27-Nov-2001 monocytogenes C;Date: 27-Nov-2001 monocytogenes C;Dates C; Pistoria C; Duchaud, E; Duchaud, A; Baquero, F; Berche, P; Bloecker; Dominguez-Bernal, G; Duchaud, E; Durand, L; Dussurget, O; Entian, K.D.; Fsihi, H. Science 294, 849-852, 2001 monocytogenes 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: E87611
R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, A.Title: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:NC 003210; PIDN:CAD00106.1; PID:g16411498; GSPDB:GN00177 A;Experimental source: strain EGD-e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GB: AE005673; NID: 913424551; PIDN: AAK24889.1; GSPDB: GN00148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             muscarinic acetylcholine receptor - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 15-Oct-1999 C;Accession: S05661, A36191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein CC2927 [imported] - Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.4%; Score 40; DB llarity 50.0%; Pred. No. 32; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||||||
KTPLTTHLTTPALIDA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 KTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:| || | || || EETELTNAVYAPVI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                            14
                                                                            ||||||| ||
PLTTAASAP 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-258 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-394 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: E87611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: 1mo2028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: CC2927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 19
                                                                                                                                                                                                        RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                         ŝ
                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
```

Gaps

ö

```
A;Cross-references: EMBL:236083; NID:g536599; PIDN:CAA85178.1; PID:g536600; MIPS:YBR214-
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Dubois, B.; El Bakkoury, M.; Glansdorff, N.; Messenguy, P.; Pierard, A.; Scherens, B. submitted to the Protein Sequence Database, August 1994
A;Reference number: 845782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 3
A;Introns: 201/3; 358/3; 424/3; 643/3; 733/3; 1014/3; 1027/3; 1178/3; 1267/3; 1313/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-1353 «ML»
A;Residues: 1-1363 «ML»
A;Cross-references: EMBL:Z93785; PIDN:CAB07859.1; GSPDB:GN00021; CESP:W09D10.2
A;Experimental source: clone W09D10
  J;Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology
                                                                                                                                                                                                                                                                                                                                                           hypothetical protein YBR214w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YBR1501
C;Species: Saccharomyces cerevisiae
C;Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 19-Apr-2002
C;Accession: S46088; S46090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein W09D10.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Rieger, M.
submitted to the Protein Sequence Database, August 1994
A;Reference number: S45734
A;Accession: Shope: DNA
A;Residues: 1-527 <RIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39; DB 2; I
Pred. No. 1.9e+02;
4; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39; DB 2;
Pred. No. 66;
                                                            DB 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 66;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, April 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 114-527 < DUB>
A;Cross-references: EMBL:Z36083; MIPS:YBR214w
A;Experimental source: strain S288C
                                                            Score 39;
Pred. No.
                                                                                                                                                                                                                                185 EKTPLTALÁTQAILERÁ 201
                                                                                                                                                                            3 EKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.18;
46.78;
                                                            48.1%;
ilarity 47.1%;
Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: SGD:SDS24
A;Cross-references: SGD:S0000418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 46...
Best Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 EEKTPLTTAAXAP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 EESTPPTATAAP 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: Z20193
                                                                                   Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Gene: CESP: W09D10.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S46090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: T26301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: T26301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 2R
                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Wall, M.
                                                                                                                                                                                                                                                                                                                                             S46088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                g
                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                        A;Accession: JQ2147
A;Accession: JQ2147
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-405 cPYS>
A;Cross-references: GB:L00623; NID:g168529; PIDN:AAA33488.1; PID:g168530
A;Experimental source: endosperm
C;Comment: This protein has a basic domain and leucine zipper domain and plays a role in C;Genetics:
A;Gene: OHP1
C;Superfamily: seed storage protein opaque-2; fos/jun DNA-binding domain homology
C;Keyworts
E;207-247/Domain: fos/jun DNA-binding domain homology <FJD>
F;233-222/Region: leucine zipper motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: B87400
B;Nierman, W.C; Feldblyum, T.V; Paulsen, I.T.; Nelson, K.E; Eisen, J.; Heidelberg, J. B;Nierman, W.C.; Elabblyum, T.V; Paulsen, R.J; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: S10772
R;Nordlund, I.; Shingler, V.
R;Nordlund, I.; Shingler, V.
Biochim. Biophys. Acta 1049, 227-230, 1990
A;Title: Nucleotide sequences of the meta-cleavage pathway enzymes 2-hydroxymuconic semi A;Reference number: S10772; MUD: 90304229; PMID: 2194577
A;Accession: S10772
A;Status: preliminary
A;Molecule type: DNA
R;Pysh, L.D.; Aukerman, M.J.; Schmidt, R.J.
Plant Cell 5, 227-236, 1993
A;Title: OHP1: a maize basic domain/leucine zipper protein that interacts with opaque2.
A;Reference number: JQ2147; MUID:93200807; PMID:8453304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reaidues: 1-507 <STO>
A;Cross-references: GB:AE005673; NID:913422542; PIDN:AAK23198.1; GSPDB:GN00148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Cross-references: EMBL:X52805; NID:g45677; PIDN:CAA36992.1; PID:g45679 C, Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology C;Keywords: oxidoreductase homology F;42-308/Domain: aldehyde dehydrogenase homology <ALDD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hydroxymuconic semialdehyde dehydrogenase (EC 1.2.1.-) - Pseudomonas putida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Species: Pseudomonas putida
;Species: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 11-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Length 405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aldehyde dehydrogenase [imported] - Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.1%; Score 39; DB 52.9%; Pred. No. 61; Live 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.0%; Score 39.5; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERKTPGTAAAASSSVVDPVEYNA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 EEKTPLTTAAXA-----PVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |:||||||
EETPLTTALLGEVMQAA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 EKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 48.0
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-486 <NOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C,Genetics:
A,Gene: CC1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
```

ò 셤

a

δ

ö

Gaps

; 0

ö

Gaps

568

g

```
C. Accession: A35125, S54397
R. Hodgson, A.L.M.; Bird, P.; Nisbet, I.T.
A. Title: Cloning, uncleotide sequence, and expression in Escherichia coli of the phosph A; Reference number: A35125, MUD: 90170833; PMID: 2407718
A; Accession: A35125
A; Accession: A35125
A; Accession: A35125
A; Accession: A35125
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-307 < HOD>
A; Molecule type: DNA
A; Residues: 1-307 < HOD>
A; Molecule type: DNA
A; Residues: 1-307 < HOD>
A; Molecule type: DNA
A; Residues: 1-307 < HOD>
A; Molecule type: DNA
A; Residues: 1-307 < HOD>
A; Molecule type: DNA
A; Residues: 1-307 < HOD>
A; Molecule type: DNA
A; Residues: 1-307 < HOD>
A; Molecule type: DNA
A; Residues: 1-307 < HOD>
A; Molecule type: DNA
A; Residues: 1-307 < HOD>
A; Molecule type: DNA
A; Residues: 1-307 < HOD>
A; Molecule type: DNA
A; Molecule 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Title: Targeted mutagenesis of the phospholipase D gene results in decreased virulence A,Reference number: S54397; MUID:95020614; PMID:7934899
A,Accession: S54397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-107 <LYN>
A;Cross-references: EMBL;AL022299; PIDN:CAA18395.1; GSPDB;GN00067; SPDB;SPBC29A3.18
A;Experimental source: strain 972h-; cosmid c29A3
C;Genetics:
            heme protein precursor - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytochrome c1 heme protein homology
cytochrome c1, heme protein precursor - fission yeast (Schizosaccharomyces p C;Species: Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jun-2000 C;Accession: T40089 R;Lyne, M; Rajandream, M.A.; Barrell, B.G.; Volckaert, G. submitted to the EMBL Data Library, March 1998 A;Reference number: Z21904 A;Reference number: Z21904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein C15H7.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: O6-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C;Accession: S40750
R;Smith, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phospholipase D (EC 3.1.4.4) precursor - Corynebacterium pseudotuberculosis C; Species: Corynebacterium pseudotuberculosis C; Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-307 <MCN>
A;Cross-references: EMBL:L16587; NID:g289915; PIDN:AAA64910.1; PID:g289916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aintrons: 20/3
C;Superfamily: cytochrome c1 heme protein; cytochrome c1 heme protein
C;Keywords: chromoportein; heme; iron; metalloprotein
C;Keywords: chromoportein; heme; iron; metalloprotein
F;71-296/Domain: cytochrome c1 heme protein homology <CIH>
F;102,105/Binding site: heme (Cys) (covalent) #status predicted
F;106/Binding site: heme iron (His) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB 2; Length 307;
Pred. No. 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38; DB 2
Pred. No. 55;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Keywords: phosphoric diester hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237 EDGTPATTAQAAKDVVN 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 EEKTPLTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 46.9%;
Similarity 61.5%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 PLTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 PVGNAAAAPVVHN 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: SPDB:SPBC29A3.18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 30
S40750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A35125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                            hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Decies: Deinococcus radiodurans
C;Decies: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: D75489
R;White, O; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamahbran, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: D75489
A;Status: preliminary
A;Residues: type: DNA
A;Residues: 1-1658 «PMI>
A;Cross-references: GB:AE001925; GB:AE000513; NID:g6458333; PIDN:AAF10268.1; PID:g645833
A;Genetics:
A;Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Pseudaletia separata
C;Species: Pseudaletia separata
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C;Accession: S68226; A39803
R;Hayakawa, Y.; Ohnishi, A.; Yamanaka, A.; Izumi, S.; Tomino, S.
R;Hayakawa, Y.; Ohnishi, A.; Yamanaka, A.; Izumi, S.; Tomino, S.
R;Hayakawa, Y.; Ohnishi, A.; Yamanaka, A.; Izumi, S.; Tomino, S.
A;Hitle: Molecular cloning and characterization of CDNA for insect biogenic peptide, grown and characterization of CDNA for insect biogenic peptide, grown and characterization of CDNA for insect biogenic peptide, grown and characterization of CDNA for insect biogenic peptide, grown and characterization of CDNA for insect biogenic peptide, grown and characterization of CDNA for insect biogenic peptide, grown and characterization of CDNA for insect biogenic peptide, grown and characterization of CDNA for insect biogenic peptide, grown and characterization of CDNA for insect biogenic peptide, grown and characterization of CDNA for insect biogenic peptide, grown and characterization of CDNA for insect biogenic peptide, grown and characterization of CDNA for insect biogenic peptide, grown and characterization of CDNA for insect biogenic peptide, grown and characterization of CDNA for insect biogenic peptide, grown and characterization of CDNA for insect biogenic peptide, grown and characterization of CDNA for insect biogenic period of control of CDNA for insect biogenic period of CDNA for insect biogenic period
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 266, 7982-7984, 1991
A;Title: Structure of a growth-blocking peptide present in parasitized insect hemolymph.
A;Reference number: A39803; MUID:91217017; PMID:2022627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-143 <HAY>
A;Cross-references: GB:S80564; NID:g1245957; PIDN:AAB35742.1; PID:g1245958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        growth-blocking peptide precursor - armyworm (Pseudaletia separata)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 121-143, YQ' < HA2>
C;Superfamily: paralytic peptide I
F;1-22/Domain: signal sequence #status predicted <SIG>
F;3-120/Domain: propeptide #status predicted <PRO>
F;23-120/Domain: propeptide #status predicted <PRO>
F;121-143/Product: growth-blocking peptide #status predicted <MAT>
F;127-139/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 143; 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
47.5%; Score 38.5; DB 2;
Best Local Similarity 58.8%; Pred. No. 2.9e+02;
Matches 10; Conservative 1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11arity 50.0%; Score 38; 12arity 50.0%; Pred. No. 2 Conservative 1; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 DEVTPATTTTTAAPAVPNA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEKTP--LTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELTPTTTVSATAPVTEN 1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 EKTPLTT-AAXAPVVXN 18
      ||::| :| | | |:
EEESPASTQASTPVM 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S68226
```

1288

ò

A;Cross-ref R;Hayakawa,

28 RESULT 7 T40089

8

ð

```
C;Accession: F81313
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hy? A;Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AL139077; GB:AL111168; NID:g6968444; PIDN:CAB73354.1; PID:g69685: A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: D71283
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwir rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDr. they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
                                                                           peptidase (M3 family) Cj1099 [imported] - Campylobacter jejuni (strain NCTC 11168)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-684 <GAT>
A;Cross-references: EMBL:U88308; PIDN:AAB42327.1; GSPDB:GN00019; CESP:C32E8.10
A;Experimental source: strain Bristol N2; clone C32E8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Introns: 24/2; 59/1; 163/3; 255/3; 282/3; 447/1; 487/1; 541/1; 587/2; 636/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T25603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable translation elongation factor G (fusA-2) - syphilis spirochete C,Species: Treponema pallidum subsp. pallidum (syphilis spirochete) C,bate: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 02-Feb-2001
                                                                                                            C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38; DB 2; Length 66%
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RjGattung, S. submitted to the EMBL Data Library, February 1997 submitted to the EMBL Data Library, February 1997 A;Description: The sequence of C. elegans cosmid C32E8. A;Reference number: Z20056 A;Accession: T25603 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein C32E8.10 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38; DB 2; I
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         487 EPENPFITAPAAPOMHNA 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: oligoendopeptidase F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 46.9%;
Local Similarity 44.4%;
es 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          385 ONTPLTTAETASV 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 EKTPLTTAAXAPV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-573 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Gene: CESP:C32E8.10
A,Map position: 1
                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                             A; Accession: F81313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: Cj1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptidase, M20/M25/M40 family [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: E87650
R;Accession: E87650
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon J.; Ernolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-474 <STO>
A;Cross-references: GB:AE005673; NID:g13424925; PIDN:AAK25201.1; GSPDB:GN00148
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F58A4.11 - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·.
                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.9%; Score 38; DB 2; Length 532; 66.7%; Pred. No. 1e+02; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 474;
                                                                                                                                                                                                                                                                              2; Length 348;
                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: $40973
A;Accession: $40983
A;Accession: $40983
A;Batuus: preliminary
A;Residues: 1-532 <BER>
A;Crose: references: EMBL: Z22179; NID:g297956; PID:g297966
C;Genetics: 82/3; 128/1; 222/1; 280/3; 397/2; 428/3; 491/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
;
submitted to the EMBL Data Library, February 1993
A;Reference number: S40750
A;Accession: S40750
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-348 <SMI>A;Crose-references: EMBL: 222173
A;Crose-references: EMBL: 222173
A;Crose-references: A;Introns: 170/1; 215/3; 297/3; 343/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, February 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38; DB 2
Pred. No. 88;
1; Mismatches
                                                                                                                                                                                                                                                                           DB
63;
                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                              Score 38;
Pred. No.
                                                                                                                                                                                                                                                                        46.9%;
nilarity 66.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.9%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           386 PLTPAIMAPIQKNA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 PLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                    :| |||| || |
229 SPCTTAASAPSV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 TPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :| |||| || |
14 SPCTTAASAPSV 25
                                                                                                                                                                                                                                                                                                                                                                                     5 TPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: E87650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: S40983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: CC3239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

Gaps

.

```
Circlession: G86194
RiTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 200
A;Authors: Hunder, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.X.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. P.; Southwick, A.M.; Sun, H.; Tallon, Rer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: F72332
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Title: Bvidence for lateral gene transfer between Archaea and Bacteria from genome se A,Reference number: A72200; MUID:99287316; PMID:10360571
A,Accession: F72332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GB:AE001747; GB:AE000512; NID:g4981304; PIDN:AAD35863.1; PID:g49813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-200 <STO>
A;Cross-references: GB:AE005172; NID:g8810460; PIDN:AAF80121.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                             hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 71;
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein - Thermotoga maritima (strain MSB8)
     4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37; DB 2;
Pred. No. 16;
5; Mismatches
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37.5;
Pred. No. 42
     4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 DELTPLAT --- APVISSA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Experimental source: strain MSB8 C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.3%;
                                                                                  346 EEEATMTTSAVSPTV 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 ORTTPVSTAGSSPVM 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 50.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 40.0
Matches 6; Conservative
                                                      2 EEKTPLTTAAXAPVV
  7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 399, 323-329, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-71 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: TM0781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 40
C83492
  Matches
                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                         ò
                                                                                                                                                                                                             C; Superfamily: translation elongation factor G; translation elongation factor Tu homolog C; Keywords: GTP binding; nucleotide binding; P-loop F;9-139/Domain: translation elongation factor Tu homology <br/>
F;15-22/Region: nucleotide-binding motif A (P-loop)<br/>
F;15-22/Region: GTP-binding NKXD motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUD19:9969613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                   A;Cross-references: GB:AE001248; GB:AE000520; NID:g3323074; PIDN:AAC65735.1; PID:g332307
E;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:Z47047; EMBL:Z38059; NID:g603997; PID:g763197; GSPDB:GN00009; MIF
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:chr_III; PIDN:CAA80127.1; PID:g3874287; GSPDB:GN00021; CESP:F58A
                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
        A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein F58A4.11 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein YIL149c - yeast (Saccharomyces cerevisiae)
C,Species: Saccharomyces cerevisiae
C,Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 19-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1679;
                                                                                                                                                                                                                                                                                                                                                                                      Length 695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 747;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                   46.9%; Score 38; DB 2; Le
llarity 60.0%; Pred. No. 1.3e+02;
Conservative 1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38; DB 2; I
Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38; DB 2; I
Pred. No. 3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, September 1994 A; Reference number: S48310 A; Accession: S48385 A; Accession: S48385 A; Molecule type: DNA A; Residues: 1-1679 < CHU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.9%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                295 EEPVTLSTDADAPVV 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Gene: SGD:MLP2, MIPS:YIL149c
A,Cross-references: SGD:S0001411
A,Map position: 9L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 SPCTTAASAPSV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 TPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity
                                                                               A; Residues: 1-695 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-747 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C, Accession: S48385
R; Churcher, C.
D71283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: F88561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: F88561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: F58A4.11
  A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
```

Gaps

ö

Gaps

· ;

```
hypothetical protein PA1228 [imported] - Pseudomonas aeruginosa (strain PA01)
C; Species: Pseudomonas aeruginosa
C; Species: Pseudomonas aeruginosa
C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C; Accession: C83492
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br Cady, S.; Olson, M.V.
Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathot A; Reference number: A82950; MUID:20437337; PMID:10984043
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-116 <STO>
A; Cross-references: GB:AE004552; GB:AE004091; NID:g9947150; PIDN:AAG04617.1; GSPDB:GN001
A; Experimental source: strain PA01
C; Genetics:
A; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB 2; Length 116;
Pred. No. 28;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 PLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:| | |||: |
54 PVTPTAAAPVIDKA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
```

Search completed: January 28, 2004, 13:09:55 Job time: 22 secs

```
EMBL; AF047025; AAC03118.1; -. EMBL; AE004841; AAG07624.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DR
DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P29342 streptonymer P4866 bordetella P1856 streptomyce P4862 bordetella P1857 agaricus bi P19059 pseudomonas P3314 saccharomyc P04665 influenza b 033367 myxococcus C2713 pseudomonas P2062 corynebacte C8cwz streptococc C8cyl pseudomonas O83748 treponema p P34478 caenorhabdi P4057 streptococc C8cyl streptococcus and C4cyl streptococcus and C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O52762 pseudomonas
P42321 proteus mir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteus mir
streptomyce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                      January 28, 2004, 13:02:49 ; Search time 11 Seconds (without alignments) 81.228 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                                                                                                                             127863
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                127863 segs, 47026705 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H2B ĀGABI
DMPC PESEP
YB64 YEAST
WUC_INBLE
GGYBB MYXXA
GBP PESES
PLD CORPS
ASSY_STRMU
CEFGI TREPA
WHA_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATA_PSEAE
CATA_PROMI
RL7_STRAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRVL
BORPE
DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YEAST
PYRWO
STRA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VIBFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOBAC
                                                                                  - protein search, using sw model
                                                                                                                                                                                                                                                       1 XEEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                 BLOSUM62 Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATA B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YIO9
FTZ1
ASSY
ASSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                      US-09-359-426C-2
81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SwissProt_41:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        695
747
1679
366
396
396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
                                                                                OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Result
```

| P18127 xanthomonas | 094051 caenorhabdi 046248 drosophila | P45459 serratia ma P19655 bacrerionba | 094620 schizosacch | O38933 alabiuopsis O88506 rattus norv P45118 haemophilus | Q8vhs6 mus musculu P07359 homo sapien |
|--------------------|---|--|--------------------|--|--|
| ICEN_XANCT | CAV1_CAEEL | DAMX_SERMA | CWFH SCHPO | SPAK RAT | AS15_MOUSE GPBA_HUMAN |
| н- | | . | | | |
| 1567 | 235 | 214 | 340 | 553 | 583 626 |
| | · 4 | 4.4 | 4.4 | . 4 . 4 | 44 |
| 45 | 45 | 4 4 | 4.4 | 4 4 4 | 4 4 |
| 37 | 36.5 | 36 | 36. | 9 9 4 | 36 |
| 34 | 36 | 98 6 | 4.0 | 4 4 4 1 0 4 | 4 4 4 5 |

ALIGNMENTS

| ###################################### | DESIGNATION OF THE STANDARD; PRT; 482 AA. COTAL PSEAE COTAL PSEAE COTAL PSEAE COTAL PSEAE COTAL PSEAE COTAL PSEAE COTAL STANDARD; PRT; 482 AA. COTAL STANDARD; PRT; 482 AA. COTAL STANDARD; PRT; 482 AA. DT 30-MAY-2000 (Rel. 39, Last sequence update) COTAL STANDARD; PRICEOBACTERIA; Semmaproteobacteria; Pseudomonadales; Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; COTAL STANDERS PROTECTIA; A. KLOZZ M. G., Nanayakkara V.K., Howell M.L., RAM MOBIL TAXIDE-287; RAM MA J.F., Cohaner U.A., KLOZZ M. G., Nanayakkara V.K., Howell M.L., RAM MA J.F., Cohaner U.A., KLOZZ M. G., Nanayakkara V.K., Howell M.L., COTAL STANDERS M. A. COTAL M. M. BITIKANDER M. C. G. T. RAM STANDERS M. A. COTAL M. M. BITIKANDER M. C. S. M. W. Z., Paulen II. M. M. RAM STANDERS M. A. COTAL M. | modified and this statement is not removed. entities requires a license agreement (See P or send an email to license@isb-sib.ch). |
|--|--|---|
|--|--|---|

DR REAL TELEFORM

```
PROSITE; PS00437; CATALASE 1; 1.
PROSITE; PS00438; CATALASE 2; 1.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide; NADP;
-!- CATALYTIC ACTIVITY: 2 H(2)0(2) = 0(2) + 2 H(2)0.
-!- COPACTOR: HEME GROUP AND NADP.
-!- SUBUNIT: Homotetramer.
-!- SUBCELLUIAR LOCATION: Cytoplasmic.
-!- MASS SPECTROMETRY: MW-55643; MW ERR=5; METHOD=Electrospray.
-!- SIMILARITY: Belongs to the catalase family.
PIR; A58663; A58663.
                                                                                                                                                                                                                                                                                                                                                                                                                                    IRON (HEME AXIAL LIGAND)
                                                                                                                                                                                                                                                                                                                                                                                METHIONINE SULFONE
                                                                                                                                PDB; IM85; 14-AUG-02.
PDB; IMQF; 09-OCT-02.
PDB; 2CAG; 07-DEC-96.
PDB; 2CAH; 11-JAN-97.
PDB; 1E93; 13-OCT-00.
InterPro; IPRO02226; Catalase.
Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
                                                                                                                                                                                                                                                                                      ProDom; PD000510; Catalase; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    443
45
45
73
73
93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1117
1119
127
138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153
156
165
167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183
185
189
194
202
205
217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219
223
235
238
238
250
251
264
269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151
151
156
158
166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233
2233
2233
224
224
224
230
330
330
330
330
330
                                                                                                                                                                                                                                                                                                                                                                                53
54
127
337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3D-structure.
MOD_RES
ACT_SITE 5
ACT_SITE 12
METAL 33
STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAND
STRAND
TURN
STRAND
TURN
HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HELLIX
TURN
STRAND
STRAND
TURN
STRAND
TURN
STRAND
TURN
HELLIX
STRAND
TURN
STRAND
TURN
STRAND
TURN
STRAND
TURN
HELLIX
HELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAND
HELIX
TURN
TURN
TURN
HELIX
TURN
TURN
TURN
TURN
TURN
           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS), AND EPR SPECTROSCOPY.
MEDLINE=21374619; PubMed=12486720;
MEDLINE=21374619; PubMed=12486730;
Andreoletti P., Sainz G., Jaquinod M., Gagnon J., Jouve H.-M.;
Hidgh-resolution structure and biochemical properties of a recombinant Proteus mirabilis catalase depleted in iron.";
Proteins 50:261-271(2003).
-!- FUNCTION: Decomposes hydrogen peroxide into water and oxygen;
serves to protect cells from the toxic effects of hydrogen peroxide.
                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INON (HEME AXIAL LIGAND) (BY SIMILARITY)
# 84E5ABA647CAB414 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=PR;
MEDLINE=95311317; PubMed=7791219;
GOUGE P. , Jouve H.-M., Dideberg O.;
"Crystal structure of Proteus mirabilis PR catalase with and without
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS), AND ABSORPTION SPECTROSCOPY.
MEDLINE=97057535; PubMed=8901874;
Gouet P., Jouve H.-M., Williams P.A., Andersson I., Andreoletti P.,
Nussaume L., Hajdu J.;
"Ferryl intermediates of catalase captured by time-resolved
Weissenberg crystallography and UV-VIS spectroscopy.";
Nat. Struct. Biol. 3:951-956(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Proteus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95305957; PubMed=7786407; Bluzy A., Bracchi V., Sterjiades R., Chroboczek J., Thibault P., Gagnon J., Jouve H.-M., Hudry-Clergeon G.; Complete amino acid sequence of Proteus mirabilis PR catalase. Occurrence of a methionine sulfone in the close proximity of the
                                                                                                                                                                                                                                                                                                                              ö
         PIR; B83113; B83113.
HSSP; P42221; 2CAE.
InterPro; IPR002225. Catalase.
Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
PRODOM; P0000510; Catalase; 1.
PROSTIE; PS00437; CATALASE.; 1.
PROSTIE; PS00438; CATALASE.; 1.
                                                                                                                                                                                                                                                                                    Score 63; DB 1; Length 482;
Pred. No. 0.0031;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Catalase (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  484 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE, AND SEQUENCE OF 1-305 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bound NADPH.";
J. Mol. Biol. 249:933-954(1995).
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . Protein Chem. 14:59-72(1995).
                                                                                                                                                                                                                                                     55589 MW;
                                                                                                                                                                                                                                                                                                                                                                   2 EEKTPLTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                        2 EEKTRLTTAAGAPVVDN 18
                                                                                                                                                                                                                                                                                        Query Match
77.8%;
Best Local Similarity 82.4%;
Matches 14; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                55
128
338
                                                                                                                                                                                                                                                     482 AA;
                                                                                                                                                                                Complete proteome.
ACT SITE 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proteus mirabilis.
                                                                                                                                                                                                 55
128
338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      active site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATA PROMI P42321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=PR;
                                                                                                                                                                                                                 ACT_SITE
METĀL
                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
CATA_PROMI
```

q

ð

m

ö

ð

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN=ATCC 10712 / ISP5230;
MEDLINE=97022081; PubMed=886841;
Facey S., Gross F., Vining L.C., Yang K., van Pee K.-H.;
"Cloning, sequencing and disruption of a bromoperoxidase-catalase gene in Streptomyces venezuelae: evidence that it is not required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X74791; CAA52796.1; -.

PIR; 837055; 837055.

RISSP; P4221; 2CAE.

InterPro; IPR002226; Catalase.

Pfam; PF00199; catalase; 1.

R PRINTS; PR0067; CATALASE.

R PROSITE; PS00437; CATALASE.

R PROSITE; PS00437; CATALASE.

R PROSITE; PS00438; CATALASE.

R Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide.

T ACT SITE 54 PS S4 BY SIMILARITY.

T ACT SITE 127 127 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces violaceus (Streptomyces venezuelae).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 43; DB 1; Length 483;
Pred. No. 7.5;
   Score 45; DB 1; Length 128; Pred. No. 0.89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          337 IRON (HEME AXIAL LIGAND) (BY 54087 MW; B58CF8230B8A2F55 CRC64;
                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1994 (Rel. 28, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Bromoperoxidase-catalase (EC 1.11.1...).
                                                                                                                                                                                                                                                                                                                                  483 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P480ē2;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
Query Match 55.6%; Score 45; DB Best Local Similarity 66.7%; Pred. No. 0.89 Matches 10; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53.1%;
69.2%;
                                                                                                                     2 EEKTPLITAAXAPVV 16
                                                                                                                                                                                28 EEKFDVTAAAAPVV 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 PLTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLTTEAGAPVADN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            483 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATA BORPE
ID CATA BORPE
AC P48062;
DT 01-FEB-1996
DT 01-FEB-1996
                                                                                                                                                                                                                                                                                                                               BCA_STRVL
P33569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                  DATE THE PRESENCE OF COLOR OF THE PRESENCE OF THE PROPERTY OF 
                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE=92380478; PubMed=1511874;

Parra F., Blanco G., Alonso J.M., Balbin M., Mendez C., Salas J.A.;

Parra F., Blanco G., Alonso J.M., Balbin M., Mendez C., Salas J.A.;

"Cloning and sequence of a gene encoding the L7/L12 ribosomal protein equivalent of Streptomyces antibioticus.";

Gene 118:127-129(1992).

-! FUNCTION: SEEMS TO BE THE BINDING SITE FOR SEVERAL OF THE PACTORS INVOLVED IN PROTEIN SYTHESIS AND APPEARS TO BE ESSENTIAL FOR ACCURATE TRANSLATION (BY SIMILARITY).

-! SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOWAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.4%; Score 53; DB 1; Length 484; 75.0%; Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 AA; 13272 MW; F5C3EE4F45D606E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55614 MW; ADC25F3CB41F5C50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 24, Created)
(Rel. 24, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam, PF00542; Ribosomal L12; T. ProDom, PD001326; Ribosomal L12; T. TIGRFAME; TIGR00855; L12; 1. Ribosomal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P02392; 1CTF.
HAMAP; MF 00368; -; 1.
InterPro; IPR000206; Ribosomal L12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50S ribosomal protein L7/L12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 EKTPLTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKKKLTTAAGAPVVDN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M89911; AAA26811.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces antibioticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JC1273; JC1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           484 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
Les 12, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-1992 (
01-DEC-1992 (
28-FEB-2003 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RL7 STRAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P29342
                                                                                                                                                 HELIX
HELIX
TURN
                                                                                                                                                                                                                                                                                                      HELIX
HELIX
                                                                                                                                                                                                                                                                                                                                                                                             TELIX
                                                                                                                                                                                                                                                                       HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
                                                                                            GRN
                                                                                                                                                                                                                                           TURN
                                                                                                                                                                                                                                                                                                                                                                                                                         TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZTRAT
```

```
722 E
78237 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49.4%;
acetylcholine receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49
60
81
100
1120
1140
1162
1162
208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   722 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27
50
61
82
101
121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119
136
147
250
                                                                                                                                                                                                                                                 TURNOVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
SO THE FERTHALL FERTHALL FERTHALL SOLD DESCRIPTION OF THE FERTHALL SOLD OF THE FERTHALL SOLD OF THE
                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HEME AXIAL LIGAND) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Oregon-R;
MEDLINE=90046926; PubMed=2510174;
Shapiro R.A., Wakimoto B.T., Subers E.M., Nathanson N.M.;
Shapiro r.A., Wakimoto functional expression in mammalian cells of "Characterization and functional expression in mammalian cells of genomic and cDNA clones encoding a Drosophila muscarinic
                                                                                                                                                                           Deshazer D., Wood G.E., Friedman R.L.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Decomposes hydrogen peroxide into water and oxygen;
serves to protect cells from the toxic effects of hydrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP, P42321, 2CAE.
InterPro; IPR00226; Catalase.
InterPro; IPR00199; catalase, 1.
PRINTS; PR00067; CATALASE.
PRODOM; PD000510; CATALASE 1.
PROSITE; PS00439; CATALASE 1; 1.
PROSITE; PS00438; CATALASE 1; 1.
Oxidoreductase; Percydase; Iron; Heme; Hydrogen peroxide.
ACT_SITE 57 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7CB73E08975C219F CRC64;
                                                                                                                                                                                                                                                 peroxide.

CATALYTIC ACTIVITY: 2 H(2)0(2) = 0(2) + 2 H(2)0.

COFACTOR: HEME GROUP.
                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to the catalase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1990 (Rel. 15, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Muscarinic acetylcholine receptor DM1.
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41;
                                                                                                                                                                                                                                                                                                       SUBUNIT: Homodimer (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IRON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1990 (Rel. 15, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54508 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U07800; AAA18481.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.6%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 LTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 LTTAAGAPVADN 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
28-FEB-2003 (Rel. 41,
Catalase (EC 1.11.1.6)
                                                   Bordetella pertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   482 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACRC OR MACR-60C
                                                                                                           NCBI_TaxID=520;
                                                                                                                                                           STRAIN=BP504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        860757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                    MEDLINE=90005981; PubMed=2507354;

MEDLINE=90005981; PubMed=2507354;

Onai T., Fitzgerald M.G., Arakawa S., Gocayne J.D., Urquhart D.A.,
Hall L.M., Fraser C.M., McCombie W.R., Venter J.C.;
"Cloning, sequence analysis and chromosome localization of a
Drosophila muscarinic acetylcholine receptor.";
FEBS Lett. 255.129-225(1989).
-: FUNCTION: THE MUSCARIOL ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,
BREAKDOWN OF PHOSPHOINOSITIERS.
                                                                                                                                                                                                                                                                                                                                                                                                                           THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING BFFECT IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interproj tracocordo 1.1.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; P800237; G PROTEIN RECEP F1 1; 1.

PROSITE; P850262; G PROTEIN RECEP F1 2; 1.

PROSITE; P850262; G PROTEIN RECEP F1 2; 1.

POSTSYNAPTIC membrane; Ionic channel; Glycoprotein; Transmembrane; Phosphorylation; Multigene family; G-protein coupled receptor.

EXTRACELIULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T -> A (IN REF. 2).
N -> S (IN REF. 2).
G -> R (IN REF. 2).
A -> AA (IN REF. 2).
P -> G (IN REF. 2).
MISSING (IN REF. 2).
G -> A (IN REF. 2).
T -> A (IN REF. 2).
C -> AR (IN REF. 2).
C -> CXS (IN REF. 2).
S -> C (IN REF. 1).
S -> C (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M27495; AAA86749.1; -.
EMBL; M23412; AAA28676.1; ALT_INIT.
PIR, S05661; 805661.
Flybase; Fbgn0000037; mACR-60C.
GO; GO:0005886; C:plasma membrane; NAS.
GO; GO:0004981; F:muscarinic acetylcholine receptor activity; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (POTENTIAL) N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB 1; Length 722;
Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPIASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FB35417CB2202A61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
Proc. Natl. Acad. Sci. U.S.A. 86:9039-9043(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 (POTENTIAL)
CYTOPLASMIC (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 (POTENTIAL)
CYTOPLASMIC (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
```

```
51682 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 EETPLTTALLGEVMQAA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 EKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 114-527 FROM N.A.
                                                                                                                                                                                                                                                                                                                     EMBL; X52805; CAA36992.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Conservative
             Proteobacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                              486 AA;
                                                                                                                                                                                                                                                                                                                                 HSSP; P20000; 1AG8
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FBR214W OR YBR1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4932;
                       NCBI_TaxID=306;
 Plasmid pVI150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=S288C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=S288c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YB64 YEAST
P38314;
                                                                                                                                                                                                                                                                                                                                                                                                                  ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                       ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
 ð
                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                Appl. Environ. Microbiol. 62:4542-4547(1996).
-!- SUBUNIT: The nucleosome is an octamer containing two molecules each of H2A, H2B, H3 and H4. The octamer wraps approximately 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
  Gaps
                                                                                                                                                                                                                                                                                                       "Isolation of expressed sequence tags of Agaricus bisporus and their assignment to chromosomes.";
                                                                                                                                                                                     Agaricus bisporus (Common mushroom).
Eukaryota; Fungi, Basidiomycota; Hymenomycetes;
Agaricales; Agaricaceae; Agaricus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00357; HISTONE H2B; 1.
Chromosomal protein; Nucleosome core; Nuclear protein; DNA-binding.
SEQUENCE 143 AA; 15165 MW; 69640102E31F4B56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
2-hydroxymuconic semialdehyde dehydrogenase (EC 1.2.1.-) (HMSD)
 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                            STRAIN=Horst U1;
MEDLINE=97111990; PubMed=8953726;
Sonnenberg A.S.M., de Groot P.W.J., Schaap P.J., Baars J.J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.1%; Score 39; DB 1; Length 143; 50.0%; Pred. No. 10;
 Indels
                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Belongs to the histone H2B family.
 7;
                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                        143 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            486 AA.
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                               van Griensven L.J.L.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, X94188; CAA63898.1; -.
InterPro; IPR004822; Histone_core.
InterPro; IPR000558; Histone_H2B.
                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , PD000497; Histone H2B; 1. SM00427; H2B; 1.
 1;
                                              EDGPTTTAAAAPLASAA 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas sp. (strain CF600)
                      3 EKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 KTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | : ||: ||| :|
11 KAPASTASKAPVKSDA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00621; HISTONEH2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00125; histone; 1
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                        STANDARD;
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                          NCBI TaxID=5341;
                                                                                                                                                                                                                                                                                                                                                                   BP of DNA
                                                                                                                           01-NOV-1997
01-NOV-1997
                                                                                                                                                                 Histone H2B.
 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSESP
                                                                                                         H2B AGABI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DMPC PS
P19059;
 Matches
                                                                                          H2B_AGABI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
                                                                                RESULT 7
                       ઠે
                                             셤
                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 엄
```

```
MEDLINE=90304229; PubMed=2194577;

MEDLINE=90304229; PubMed=2194577;

Mordlund I., Shingler V.; Aningler V.; Shingler V.; Sequences of the meta-cleavage pathway enzymes 2-hordroxymuconic semialdehyde dehydrogenase and 2-hydroxymuconic semialdehyde hydrolase from Pseudomonas CF600."; Semialdehyde hydrolase from Pseudomonas CF600."; Semialdehyde hydrolase from Pseudomonas CF600."; Semialdehyde Acta 1049:227-230(1990).

-!- FUNCTION: 2-HYDROXYPHCONIC ACID SEMIALDEHYDE CAN BE CONVERTED TO 2-HYDROXYPHUCONIC SEMIALDEHYDE HYDROLASE (HWSH) OR BY THE ACTION OF THREE SEQUENTIAL ENZYMES, THE FIRST OF WHICH IS HMSD.

-!- PATHWAY: META-CLEAVAGE PATHWAY FOR THE DEGRADATION OF PHENOLS, CRESOLS AND CATECHOL, PHENOL METABOLISM.

CRESOLS AND CATECHOL. PHENOL METABOLISM.

CRESOLS AND CATECHOL. PHENOL METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dubois E., el Bakkoury M., Glansdorff N., Messenguy F., Pierard A., Scherens B., Vierendeels F.; Submitted (Aug-1994) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO YEAST YGL056C AND S.POMBE SDS23.
-!- SIMILARITY: Contains 2 CBS domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IDR002086; Aldehyde_dehydr.
Pfam; PF00171; aldedh; 1.
PROSITE; PS001070; ALDEHYDE_DEHYDR_CYS; 1.
PROSITE; PS001687; ALDEHYDE_DEHYDR_GLU; 1.
Aromatic hydrocarbons catabolism; Oxidoreductase; NAD; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-UTL-1998 (Rel. 36, Last amortation update)
Hypothetical 57.2 kDa protein in MET8-HPC2 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rieger M.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F906FCA64185AA68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.1%; Score 39;
52.9%; Pred. No. 3
```

; 0

Gaps

; 0

7; Indels

Mismatches

```
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=34;
                                                                                                                                                                                                        GYRB MYXXA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                             033367
                                                                                                                                                                               GYRB_MYXXA
  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                      d
                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb'sib.ch/announce/
                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Briedis D.J., Tobin M.;
"Influenza B virus genome: complete nucleotide sequence of
influenza B/lee/40 virus genome RNA segment 5 encoding the
nucleoprotein and comparison with the B/Singapore/222/79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Influenza B virus (strain B/Lee/40).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: ENCAPSIDATES THE NEGATIVE STRAND VIRAL RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              527 AA; 57187 MW; DC2741550A69C154 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   560 AA; 61770 MW; 74C4FEAF9E75A695 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.1%; Score 39; DB 1;
61.5%; Pred. No. 39;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39; DB 1;
Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-1987 (Rel. 05, Last sequence update) 01-MAY-1992 (Rel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00571; CBS; 4. —
WARAT; SM00116; CBS; 2. Hypothetical protein; Repeat; CBS domain. DOMAIN 196 251.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                              SGD; S0000418; SDS24.
GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0006259; P:DNA metabolism; IGI.
GO; GO:0006897; P:endocytosis; IMP.
GO; GO:0007126; P:meiosis; IEP.
InterPro; IPR000644; CBS_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=84174071; PubMed=6324462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-AUG-1987 (Rel. 05, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48.18;
                                                                                                                                                                                                        EMBL; Z36083; CAA85178.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro, IPR002141, Flu_NP.
Pfam, PP00506, Flu_NP, 1.
Nucleoprotein.
SEQUENCE 560 AA, 61770 MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 61.5%;
nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; K01395; AAA43689.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleoprotein.";
Virology 133:448-455(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 EEKTPLTTAAXAP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 EESTPPTATAAAP 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                  PIR; S46088; S46088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=11535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VNUC INBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P04665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VNUC_INBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
       SO THE PRESENTATION OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Paitan Y., Boulton N., Ron E.Z., Rosenberg E., Orr E.;
"Molecular analysis of the DNA gyrB gene from Myxococous xanthus.";
"Microbiology 144:1641-1647(1998)
"Interconsisting of the DNA BARABE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE-STRANDED DNA IN AN ATP-DEPENDENT WANNER AND ALSO CATALYZES THE INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED DNA RINGS, INCLUDING CATENANES AND KNOTTED RINGS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SUBUNIT; MADE UP OF TWO CHAINS. THE A CHAIN IS RESPONSIBLE FOR DAY BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE ENZYME FORMS AN A2B2 TETRAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining of double-stranded DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
Cystobacterineae; Myxococcaceae; Myxococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Belongs to the type II topoisomerase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39; DB 1; Length 815;
Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGRFAMS; TIGR01059; gyrB; 1.
PROSITE; PS00177; TOPOISOMERASE II; 1.
TOPOISOMERASE; ISOMERASE; ISOMERASE; ISOMERASE; SEQUENCE 815 AA; 89636 MW; 3862685FBB805B32 CRC64;
                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA gyrase subunit B (EC 5.99.1.3).
                                                                                                                                                                                                                                                                                                 815 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AJ000543; CAA04176.1; -...
HSSP, P06982; 1AJ6.
INTECPTO; IPRO013594; ATPDING ATPASE.
INTECPTO; IPRO013594; ATPDING ATPASE.
INTECPTO; IPRO01241; DNA LOPDISOII.
INTECPTO; IPRO01241; DNA LOPDISOII.
INTECPTO; IPRO06171; TOPTIM dom.
Pfam; PF00186; DNA GyraseB; 1.
Pfam; PF00186; DNA GyraseB; 1.
Pfam; PF01751; TOPTIM; 1.
PRINTS; PR00418; TPIZPAMILY.
PROD0187; HATPASE C; 1.
SMART; SM00433; HATPASE C; 1.
SMART; SM00433; HATPASE C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=ER-15;
MEDLINE=98304088; PubMed=9639935;
٠,
س
                                                                 2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                               19 EELTPGTSGATRPIIKPA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 66.7
es 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14
                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 EKTPATGSAVAP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myxococcus xanthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

-

```
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide.";
J. Biol. Chem. 274:1887-1890(1999).
J. Biol. Chem. 274:1887-1890(1999).
J. Biol. Chem. 274:1887-1890(1999).
ONSET OF METAMORPHOSIS FROM LARVA TO PUPA. THIS GROWTH-BLOCKING PEPTIDE HAS REPRESSIVE ACTIVITY AGAINST JUVENILE HORMONE ESTERASE.
SIMILARITY: BELONGS TO THE GBP / PSP1 / PARALYTIC PEPTIDE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aizawa T., Fujitani N., Hayakawa Y., Ohnishi A., Ohkubo T., Kumaki Y.,
                                                                                                  15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-EB-2003 (Rel. 41, Last annotation update)
Growth-blocking peptide precursor (GBP).
Pseudaletia separata (Armyworm).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Noottera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
NCEL TaxID=7105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=96105377; PubMed=7498538;
Hayakawa Y., Ohnishi A., Yamanaka A., Izumi S., Tomino S.;
"Molecular cloning and characterization of cDNA for insect biogenic Peptide, growth-blocking peptide.";
FEBS Lett. 376:185-189(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayakawa Y., Noguchi H.; "Growth-blocking peptide expressed in the insect nervous system: "Growth-blocking peptide closing and functional chracterization."; Eur. J. Biochem. 253:810-816(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kawano K., Hikichi K., Nitta K.; "Solution structure of an insect growth factor, growth-blocking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15256 MW; DEBFB527956840EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GROWTH-BLOCKING PEPTIDE.
                                                                                           143 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Hemolymph;
MEDLINE=99107831; PubMed=9890941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=98316655; PubMed=9654083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF02425; GBP PSP; I.
ProDom; PD006507; GBP PSP; 1.
Hemolymph; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB012294; BAA32793.1; -. PIR; S68226; S68226.
PDB; 1BQF; 09-DEC-98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR003463; GBP_PSP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; S80564; AAB35742.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRUCTURE BY NMR OF 121-143.
                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 AA;
                                                                                 GBP_PSESE
Q27913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEPTIDE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROPEP
                      RESULT 12
GBP_PSESE
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          decreased virulence of Corynebacterium pseudotuberculosis.";
Mol. Microbiol. 12:921-930(1994)
-!- FUNCTION: VIRULENCE FACTOR AFFECTING BACTERIAL DISSEMINATION AND
-:- SURVIVAL WITHIN THE HOST. HAS MAGNESIUM-DEPENDENT SPHINGOMYELINASE
                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 25-47.

MEDLINE=90170833; PubMed=2407718;
Hodgson A.L.M., Bird P., Nisbet I.T.;
"Cloning, nucleotide sequence, and expression in Escherichia coli of the phospholipase D gene from Corynebacterium pseudotuberculosis.";
J. Bacteriol. 172:1256-1261(1990).
                               P20626; Q59314;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Phospholipase D precursor (EC 3.1.4.4) (PLD) (Choline phosphatase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- CATALYTIC ACTIVITY: A phosphatidylcholine + H(2)0 = choline + a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=Biovar equi'/ Isolate 155;
MEDLINE=9525563; PubMed=7737503;
MCNamara P.J., Cuevas W.J., Songer J.G.;
"Toxic phospholipases D of Corynebacterium pseudotuberculosis, Culterans and Arcanobacterium haemolyticum: cloning and sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Blovar ovis / Isolate Whetten 1;
MEDINE=5920614; PubMed=7934899;
MRONanara P.J., Bradley G.A., Songer J.G.;
"Targeted mutagenesis of the phospholipase D gene results in
                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase, Lipid degradation, Magnesium, Virulence, Signal.
SIGNAL 1 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phosphatidate.
-!- SIMILARITY: TO OTHER CORYNEBACTERIUM PHOSPHOLIPASES D.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Songer J.G., Libby S.J., Iandolo J.J., Cuevas W.A., "Cloning and expression of the phospholipase D gene from Corynebacterium pseudotuberculosis in Escherichia coli."; Infect. Immun. 58:131-136(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHOLIPASE D.
               307 AA
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=Biovar ovis / Isolate Whetten 1;
MEDLINE=90093451; PubMed=2403529;
               PRT;
                                                                                                                                                   Corynebacterium pseudotuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L16587; AAA64910.1; -.
EMBL; L16586; AAA99867.1; -.
PIR; A35125; A35125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND HEMOLYTIC ACTIVITY
                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene 156:113-118(1995).
                                                                                                                                                                                                             NCBI_TaxID=1719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [4]
MUTAGENESIS.
                 PLD CORPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
PLD_CORPS
```

7

Gaps

5;

Indels

46.9%; Score 38; DB 1; Length 143; 50.0%; Pred. No. 15;

1; Mismatches

Conservative

Matches

Local Similarity 10;

Query Match

FT FT S

ò

```
EMBL; U63511; AAB88219.1; -. HSSP; P42321; 2CAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 66.7
les 8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 LTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 LTTASGAPVADN 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                putida.";
Gene 199:219-224(1997)
                                                                                                                                                                                                                                                    Pseudomonas putida
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Corvallis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126
336
                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EFG1 TREPA
083748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peroxide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EFG1_TREPA
                               CATA_PSEPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 16
                                                            A PART OF THE PROPERTY OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation her buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=UAIS9 / ATCC 700610 / Serotype C;
MEDLINE=22295063; PubMed=12397186;
Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Primeaux C., Tain R., Kenton S., Jia H., Lin S., Qian Y.,
Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti J.J.;
"Genome sequence of Streptococcus mutans UAIS9, a cariogenic dental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                             Gaps
E -> G (IN BIOVAR EQUI / ISOLATE 155)

N -> D (IN BIOVAR EQUI / ISOLATE 155)

I -> M (IN BIOVAR EQUI / ISOLATE 155)

A -> P (IN BIOVAR EQUI / ISOLATE 155)

D3B1334E6FC99975 CRC64;

    Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
    -!- CATALYTIC ACTIVITY: ATP + L-citrulline + L-aspartate = AMP + diphosphate + L-argininosuccinate.
    -!- PATHMAY: Arginine blosynthesis; seventh step.
    -!- SUBUNT: Homotectramer (By similarity).
    -!- SUBUNT: Belongs to the argininosuccinate synthase family.

                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Argininosuccinate synthase (EC 6.3.4.5) (Citrulline--aspartate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP; MF 00005; -; 1.

Pfam; PF00764; Arginosuc synth; 1.

ProDom; PD003544; Arginosuc synth; 1.

TIGRFAMs; TICR00032; argG; 1.

PROSITE; PS00564; ARGININOSUCCIN SYN 1; 1.

PROSITE; PS00565; ARGININOSUCCIN SYN 2; 1.

Arginine biosynthesis; Lidase; AFP-binding; Complete proteome. SEQUENCE 396 AA, 43913 MW; 44A7C6D56865137E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38; DB 1; Length 396;
Pred. No. 43;
3; Mismatches 5; Indels
                                                                                                                                                                       DB 1; Length 307;
                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus mutans.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                396 AA
                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                       Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-SEP-2003 (Rel. 42, Created)
                                                                                                                   33884 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE014881; AAN58093.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.98;
                                                                                                                                                                    Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQKYPLVSALSRPVI 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 46.7°
Matches 7; Conservative
                                                                                                                                                                                                                                                                                    6 PLTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                        18 PVGNAAAAPVVHN 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                               205
270
277
     189
205
270
270
277
307 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Subfamily 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ilgase/.
ARGG OR SMU.334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pathogen.'
     VARIANT
VARIANT
VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QBCWZO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1gase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASSY STRMU
```

8 g

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    336 336 IRON (HEWE AXIAL LIGAND) (BY SIMILARITY) 479 AA, 53381 MW; EFE3CBDE67778571 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC.1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Elongation factor G 1 (EF-G 1).
FUSA OR FUSA-2 OR TP0767.
Treponema pallidum.
Bacteria, Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
NCBI_TAXID=160;
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98019091; PubMed=9358059;
Kim Y.C., Miller C.D., Anderson A.J.;
"Identification of adjacent genes encoding the major catalase and
bacterioferritin from the plant-beneficial bacterium Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- FUNCTION: Decomposes hydrogen peroxide into water and oxygen; serves to protect cells from the toxic effects of hydrogen
                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide.
ACT SITE 53 53 BY SIMILARITY.
ACT_SITE 126 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB 1; Length 479;
Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
-!- COFACTOR: HEME GROUP.
-!- ENZIYER REGULATION: ACTIVATED BY PEROXIDE.
-!- SIMILARITY: Belongs to the catalase family.
JO-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Catalase (EC 1.11.1.6).
RATA OR CATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         695 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IRR00226; Catalase.
Pfam; PF00199; Catalase; 1.
PRINTS; PR00067; CATALASE.
PRODOM; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE 1; 1.
PROSITE; PS00438; CATALASE 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OC CON CONTRACTOR
```

ပ

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                                                                                                                                                                                        Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Rooper A., Sanuders D., Shownkeen R.,
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer B., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Wateson A., Weinstock L., Wilkinson-Sproat J.,
                      Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Hypothetical 195.1 kDa protein in DNA43-UBI1 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=S288c / AB972;
PubMed=9169870;
Churcher C.M., Bowman S., Badcock K., Bankier A., Brown D.,
Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB 1; Length 747; Pred. No. 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     747 AA; 83221 MW; 23890C5F8DCFFB15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Contains 2 BED-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1679 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Repeat; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BED-TYPE 1.
BED-TYPE 2.
                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE-94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, Z22179, CAA80127.1; JOINED.
EMBL, Z22179, CAA80171.1; -.
EMBL, Z22173; CAA80171.1; JOINED.
PIR, F88561; F88561.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WormPep; F58A4.11; CE00217.
InterPro; IPR003656; BED_finger.
PROSITE; PS50808; ZF_BED; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z22173; CAA80127.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|||||||||
229 SPCTTAASAPSV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 TPLTTAAXAPVV.16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 368:32-38(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4932;
                                                                                       NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YIO9_YEAST
ID _YIO9_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P40457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YIL149C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
      d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                Science 281:375-388(1998).
-!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT TRANSLOCATION
OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
                                                                                                                       Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gainn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren. E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T. McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O. Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 46.9%; Score 38; DB 1; Length 695; Best Local Similarity 60.0%; Pred. No. 76; Matches 9; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pram; Proof 19, EFG C, 1.
Pram; Proof 9, EFG C, 1.
Pram; Proof 4, EFG IV, 1.
Pram; Proof 4, EFG IV, 1.
Pram; Proof 5, EFG IV, 1.
Pram; Proof 5, EFG IV, 1.
Pram; Proof 5, EFG IV, 1.
Proof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46529989BFE97E4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein F58A4.11 in chromosome III:
F58A4.11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              747 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAWAR, MF 00054; -; 1.
INTERPRO; IPR004540; EF-G.
INTERPRO; IPR000795; EF GTPbind.
INTERPRO; IPR000640; EFG_C.
INTERPRO; IPR005517; EFG_IV.
INTERPRO; IPR005517; EFG_IV.
INTERPRO; IPR005525; Small_GTP.
                                                                                   MEDLINE=98332770; PubMed=9665876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE001248; AAC65735.1; -. PIR; D71283; D71283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76831 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      295 EEPVTLSTDADAPVV 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EF-G/EF-2 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P13551; 2EFG.
TIGR; TP0767; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 695 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIBOSOME
                                                                                                                                                                                                                                                                                                                                                                         spirochete.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YMHA CAEEL
P34478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NP_BIND
SEOUENCE
```

ö

YMHA_CAEEL RESULT 17

SEATER

g

ठ

```
Subfamily 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARGG OR GBS0123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                            STRA3
                                                                                                                         NP BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kunst F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                  QBE7N1;
                                                                                                                                                                                                                                                                                                                                                                                                                                 ASSY
                                                                                                                                                                                                                                                                                                                                                                                     RESULT 20
                                                                                                                                                                                                                                                                                                                     엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STABBBBB
                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@18b-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lye G., Moule S., Odell C., Peargon D., Rajandream M.A., Rice P., Rowley N., Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G.; "The nucleotide sequence of Saccharomyces cerevisiae chromosome IX."; "The nucleotide sequence of Saccharomyces cerevisiae chromosome IX.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pyrococcus woesei.
Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.9%; Score 38; DB 1; Length 1679;
46.7%; Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  195141 MW; 298950CC52202D8F CRC64;
                                                                                                                                                                                                                                                                                                                                                              GO:0005635; C:nuclear membrane; IDA.
GO:0005654; C:nucleoplasm; IDA.
GO:0006606; P:protein-nucleus import; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
FTSZ1 OR FTSZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  366 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000158; FtsZ.
InterPro; IPR003008; Tubulin FtsZ.
                                                                                                                                                                                                                                                                                              EMBL; Z38059; CAA86129.1; -. PIR; S48385; S48385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U56247; AAA99162.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||: :||:| EEEATMTTSAVSPTV 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003008; Tubul
Pfam; PF00091; tubulin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 46.7
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                   Nature 387:84-87(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
SEQUENCE 1679 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q57816; 1FSZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pyrococcus.
NCBI_TaxID=2262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PYRWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FTZ1 PY
Q52630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 19
FTZ1 PYRWO
                                                                                                                                                                                                                                                                                                                                             SGD;
    RARA RARA BARA DIR BA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=NEM316 / Serctype III;
MEDLINE=2224508; PubMed=12354221;
Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek I., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diphosphate + L-argininosuccinate.
-!- PATHWAY: Arginine biosynthesis; seventh step.
-!- SUBUNIT: Homotetramer (By similarity).
-!- SIMILARITY: Belongs to the argininosuccinate synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of Streptococcus agalactiae, a pathogen causing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invasive neonatal disease.";
Mol. Microbiol. 45:1499-1513(2002).
-!- CATALYTIC ACTIVITY: ATP + L-citrulline + L-aspartate = AMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [5-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Argininosuccinate synthase (EC 6.3.4.5) (Citrulline--aspartate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGEFAMS; TIGENO002: argG; I.
PROSITE; PS00564; ARGININOSUCCIN SYN 1; 1.
PROSITE; PS00565; ARGININOSUCCIN SYN 2; 1.
Arginine biosynthesis; Ligase; ATP-binding; Complete proteome. SEQUENCE 396 AA; 43725 MW; 31DB024B0785AC52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.7%; Score 37; DB 1; Length 396; 40.0%; Pred. No. 63; 5; Indels tive 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                     Length 366;
                                                                                                                                                                                                                                                                                                                                                                                           Indels
Pfam, PF03953; tubulin_C; 1.
PRINTE, PR00423; CELLD/18FFSZ.
TIGRPAMS; TIGR00065; ftez; 1.
PROSITE; PS01134; FTSZ_1; 1.
PROSITE; PS01135; FTSZ_2; 1.
PROSITE; PS01136; FTSZ_2; 1.
PROSITE; PS01135; FTSZ_2; 1.
PROSITE; PS01135; FTSZ_2; 1.
PROSITE; PS01135; FTSZ_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus agalactiae (serotype III).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae;
                                                                                                                                                                                                               128 136 GTP (POTENTIAL).
366 AA; 39511 MW; 8B40594318F955BFF CRC64;
                                                                                                                                                                                                                                                                                                              Query Match
45.7%; Score 37; DB 1;
Best Local Similarity 46.7%; Pred. No. 59;
Matches 7; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 396 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sagailst; gb80123; -.
HAMAP; MF 00005; -; 1.
InterPro; IPR001518; Arginosuc_synth.
Pfam; PF00764; Arginosuc_synth; 1.
ProDom; PD0003544; Arginosuc_synth; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AL766843; CAD45768.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  345 EEETPLETPEESPSI 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 40.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=216495;
```

```
30-MAY-2000
                                      30-MAY-2000
                                                    16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATA_VIBFI
ID CATA_VIBFI
AC O68146;
SDC3 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
               064519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 23
 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Lucypean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                          STRAIN=2603 V/R / Serotype V;
MEDLINE=2222988; pubMed=12200547;
MEDLINE=2222988; pubMed=12200547;
Fettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S., Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D., Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R., Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S., Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M., Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D., Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PATHWAY: Arginine biosynthesis; seventh step.
-!- SUBUNIT: Homotetramer (By similarity).
-!- SIMILARITY: Belongs to the argininosuccinate synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                            'Complete genome sequence and comparative genomic analysis of an
                                                                                                                                                                                                                                                                                                                                                                                                                                      emerging human pathogen, serotype V Streptococcus agalactiae.";
Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396 (2002).
-!- CATALYTIC ACTIVITY: ATP + L-citrulline + L-aspartate = AMP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                              15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Argininosuccinate synthase (EC 6.3.4.5) (Citrulline--aspartate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP; MF_00065; -; 1.

InterPro; IPR001518; Arginosuc_synth.

Promis - Pr00764; Arginosuc_synth; 1.

ProDom; P0003544; Arginosuc_synth; 1.

TIGRFAMS; TIGR00032; argg; 1.

PROSITE; PS00564; ARGININOSUCCIN_SYN 1; 1.

PROSITE; PS00565; ARGININOSUCCIN_SYN 2; 1.

Arginine blosynthesis; Ligase; ATP-binding; Complete proteome. SEQUENCE 396 AA; 43697 MW; 31CAC841B6E5AC52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                               Streptococcus agalactiae (serotype V).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         π̈́
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37; DB 1
                                                                                         396 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 63;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diphosphate + L-argininosuccinate.
                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE014197; AAM99033.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.7%;
EEKTPLTTAAXAPVV 16
               |:| || :| |::
82 EQKYPLVSALSRPII 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 EQKYPLVSALSRPII 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                       NCBI_TaxID=216466;
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Subfamily 1.
                                                                                                                                                                                   ARGG OR SAG0125.
                                                                                                                                                                                                                           Streptococcus
                                                                                         STRAS
N
                                                                                                  Q8E272;
                                                                                                                                                                         igase)
                                                                           STRAS
                                                                                         ASSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
ò
                       셤
                                                                                                      d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
```

RESULT 22 SDC3_MOUSE

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL). (POTENTIAL). (POTENTIAL).
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN=C57BL/6 X CBA;

Kung C.E., Deuel T.F.;

Kung C.E., Deuel T.F.;

**Cloning of rat and meuse syndecan-3 cDNAs.";

submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- PTM: O-GLYCOSYLATED WITHIN THE THRYSER-RICH REGION WHICH COULD INTERACT WITH LECTIN DOMAINS ON OTHER MOLECULES (PROBBALE).

-!- SIMILARITY: BELONGS TO THE SYNDECAN FAMILY OF INTEGRAL MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proteoglycan; Heparan sulfate; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CLENYGE OF ECTODOMAIN (POTENTIAL).
O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIO-LINKED (GLYCOSAMINOGLYCAN) (POTENTIO-LINKED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB 1; Length 442;
Pred. No. 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D2F1CE6E611FA164 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL)
                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
catalase (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              482 AA
  442 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD, MGI:1349163; Sdc3.
InterPro; IPR003585; Neurexin-like.
InterPro; IPR001050; Syndecan.
Pfam; PP01034; Syndecan; 1.
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00294; 4.1m; 1.
PROSITE; PS00964; SYNDECAN; 1.
                                               (Rel. 39, Created)
(Rel. 39, Last seq
(Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46101 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U52826; AAB03283.1; -.
                                                                                                                        Syndecan-3 precursor (SYND3)
SDC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 PLTTAATAKITTPA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 PLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 57.1
nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  384
4409
3002
3002
78
80
80
80
82
83
315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        367
                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               442 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEOGLYCANS.
                                                                                                                                                                                                                                                NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SE DI DI BE
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                       "Metabolism of cyclic carotenoids: a model for the alteration of this biosynthetic pathway in Capsicum annuum chromoplasts."; plant 7424(1985).
-!- FUNCTION: CATALYZES THE DOUBLE CYCLIZATION REACTION WHICH CONVERTS LYCOPENE TO BETA-CAROTENE AND NEUROSPORENE TO BETA-ZEACAROTENE.
-!- PATHWAY: Carotenoid biosynthesis.
-!- SUBCELLULAR LOCATION: Chloroplast, chromoplast.
-!- SUBCELLULAR LOCATION: Of THE LYCOPENE CYCLASE FAMILY.
                                                             Hugueney P., Badillo A., Chen H.C., Klein A., Hirschberg J., Camara B., Kuntz M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oxidoreductase; NAD; Carotenoid biosynthesis; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.7%; Score 37; DB 1; Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 498 LYCOPENE BETA CYCLASE.
84 112 NAD (POTENTIAL).
498 AA; 55610 MW; 177180CD5745F64F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHLOROPLAST (POTENTIAL) .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                              EMBL, X86221; CRA60119.1; -.
InterPro; IPR001327; FAD pyr redox.
InterPro; IPR00205; NAD_binding.
InterPro; IPR00100; Pyr_redox.
                           STRAIN=cv. Lamuyo; TISSUB=Fruit;
MEDLINE=96045549; PubMed=7550379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00368; FADPNR. PRINTS; PR00411; PNDRDTASEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              370 TLAAAPVVANA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 TAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transit peptide.
TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LCY1 OR CRTL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ONIE GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gantt E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          043503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 25
LCYB_LYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ong as its content is in no way loved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                               "The periplasmic, group III catalase of Vibrio fischeri is required
"The periplasmic, group III catalase of Vibrio fischeri is required
for normal symbiotic competence and is induced both by oxidative
for normal symbiotic competence and is induced both by oxidative
for stress and by approach to stationary phase.";

"Bacteriol. 180:2087-2092(1998)

"EDINITION: Decomposes hydrogen peroxide into water and oxygen;
serves to protect cells from the toxic effects of hydrogen
peroxide. Could protect cells in nodules which have a high
peroxide. Could protect cells in nodules which have a high
peroxide conditions required for nitrogen fixation and the action
of several proteins.

"CATALYTIC ACTIVITY: 2 H(2)(2) = 0(2) + 2 H(2)(2).

"CATALYTIC ACTIVITY: 2 H(2)(2) = 0(2) + 2 H(2)(2).

"COPACTOR: HEME GROUP.

"COPACTOR: HEME GROUP.

"INDUCTION: By hydrogen peroxide.

"INDUCTION: By hydrogen peroxide.

"HISCELLANEOUS: EITHER KATA OR KATC IS ABSOLUTELY REQUIRED FOR THE
PROTECTION OF THE NITROGEN FIXATION PROCESS.

"INDUCTION: BY HYGROGEN FIXATION PROCESS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
BY SIMILARITY.
SIMILARITY.
13808F0DBDE4DCG32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Capsicum annuum (Bell pepper).

Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Bopermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae, lamiids; Solanales; Solanaceae; Capsicum.

NCBL_TaxID=4072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Lycopene beta cyclase, chloroplast precursor (EC 1.14.-.-).
             Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD000510; Catalase; 1.
PROSITE; PS00437; CAPALASE 1; 1.
PROSITE; PS00438.
Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB 1; Length 482; Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     498 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                    MEDLINE=98215175; PubMed=9555890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF011784; AAC38344.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002226; Catalase.
Pfam; PF00199; catalase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54864 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00067; CATALASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 LTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LTTAAGCPVAHN 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               482 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                   SEQUENCE FROM N.A.
                                                    NCBI_TaxID=668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P42321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LCY1 OR CRTL.
                                                                                                     STRAIN=ES114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Periplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LCYB CAPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  043415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LCYB_CAPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 24
   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
```

Gaps

.; 0

3; Indels

```
formation.";
Plant Cell 8:1613-1626(1996).
-!- FUNCTION: CATALYZES THE DOUBLE CYCLIZATION REACTION WHICH CONVERTS
-!- FONCTION: CATALYZES THE DOUBLE CYCLIZATION REACTION WHICH CONVERTS
-!- PATHWAY: Carotemoid biosynthesis.
-!- SUBCELLULAR LOCATION: Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CV. VF36; TISSUE=Leaf;
MEDLINE=96434545; PubMed=8837512;
Cunningham F.X. Jr., Pogson B., Sun Z., McDonald K.A., Dellapenna D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Functional analysis of the beta and epsilon lycopene cyclase enzyme of Arabidopsis reveals a mechanism for control of cyclic carotenoid
                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                          Lycopene beta cyclase, chloroplast precursor (EC 1.14.-.-).
                                                                                                                                                                   (Rel. 41, Last annotation update)
500 AA
                                                                                                                             Last sequence update)
                                                                                                                                                                                                                                                                                            Lycopersicon esculentum (Tomato).
                                                                                      16-OCT-2001 (Rel. 40, Created)
```

```
82
86
                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=StMa]
                                                                                                                                                                                                                                                  PSD3 ANOST
Q9U5Z8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proteasome.
SEQUENCE
                                                                NP BIND
SEQUENCE
                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                     CHAIN
                                                                                                                                                                                                                                        PSD3_ANOST
                                                                                                                                Matches
                                                                                                                                                                                                                          RESULT
  SFFFF
                                                                                                                                                          ò
                                                                                                                                                                                 d
                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             formation.";
Plant Cell 8:1613-1626(1996).
-!- FOUNCTION: CATALYZES THE DOUBLE CYCLIZATION REACTION WHICH CONVERTS
LYCOPENE TO BETA-CAROTENE AND NEUROSPORENE TO BETA-ZEACAROTENE.
-!- PATHWAY: Carotenoid biosynthesis.
-!- SUBCELLULAR LOCATION: Chloroplast.
-!- SUBCELLULAR LOCATION: Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=cv. Samsun NN; TISSUE=Leaf;
MEDLINE=96434545; PubMed=8837512;
Cunningham F.X. Jr., Pogson B., Sun Z., McDonald K.A., Dellapenna D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Functional analysis of the beta and epsilon lycopene cyclase enzymes of Arabidopsis reveals a mechanism for control of cyclic carotenoid
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Asteridae, lamiids, Solanales, Solanaceae, Nicotiana.
                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lylopene beta cyclase, chloroplast precursor (EC 1.14.-.-).
LCY1 OR CRIL-1.
                                                                                                                                                                                            PRINTS; PR00368; FADPR. -
PRINTS; PR00411; PNDRDTASEI.
Oxidoreductase; NAD; Carotenoid biosynthesis; Chloroplast;
                                                                                                                                                                                                                                                                                                                   DB 1; Length 500;
                                                                                                                                                                                                                                                                                                                                               3; Indels
 -!- SIMILARITY: BELONGS TO THE LYCOPENE CYCLASE FAMILY.
                                                                                                                                                                                                                                                                                        CF42F7D4684C04DD CRC64;
                                                                                                                                                                                                                                               CHLOROPLAST (POTENTIAL).
LYCOPENE BETA CYCLASE.
NAD (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                500 AA
                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                 Pred. No. 80;
                                                                                          entities requires a license agreement (Son send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                   Score 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional analysis of the beta and
                                                                                                                                                      InterPro; IPR001327; FAD pyr redox.
InterPro; IPR001205; NAD binding.
InterPro; IPR001100; Pyr_redox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nicotiana tabacum (Common tobacco)
                                                                                                                                                                                                                                                                                         56180 MW;
                                                                                                                                                                                                                                                                                                                45.7%;
72.7%;
                                                                                                                                EMBL; X86452; CAA60170.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X81787; CAA57386.1; -.
PIR; S72506; S72506.
                                                                                                                                                                                                                                                                                                                                             8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              372 TLAAAPVVANA 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                       9 TAAXAPVVXNA 19
                                                                                                                                                                                                                                                   81
500
114
                                                                                                                                               S72505; S72505.
                                                                                                                                                                                                                                                                                         500 AA;
                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4097;
                                                                                                                                                                                                                                     Fransit peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOBAC
                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                            NP BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        043578;
                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 26
LCYB_TOBAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gantt
                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                            Matches
ò
                                                                                                                                                                                                                                                                                                                                                                                              d
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Garvey C.F., Malcolm C.A.;
"Anopheles stephensi Dox-A2 shares common ancestry with genes from distant groups of eukarryctes encoding a 265 proteasome subunit and is in a conserved gene cluster."

J. Mol. Evol. 50:497-509(2000).

-!- FUNCIVED IN THE ATP-DEPENDENT DEGRADATION OF UBIQUITINATED PROTEINS (BY SIMILARITY).

-SUBUNIT: THE 265 PROTEASOME IS COMPOSED OF A CORE PROTEASE, KNOWN AS THE 205 PROTEASOME, CAPPED AT ONE OR BOTH ENDS BY THE 195 REGULATORY COMPLEX (RC). THE RC IS COMPOSED OF A LEAST 18

DIFFERENT SUBUNITS IN TWO SUBCOMPLEXES, THE BASE AND THE LID,
WHICH FORM THE PORTITIONS PROXIMAL AND DISTAL TO THE 205 PROTECLYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORE, RESPECTIVELY (BY SIMILARITY).

-!- DOMAIN: CONTAINS 1 PCI DOMAIN.

-!- SIMILARITY: BELONGS TO THE PROTEASOME SUBUNIT S3 FAMILY.

-!- CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO BE THE DIPHENOL OXIDASE

A2 COMPONENT INVOLVED IN CATECHOLAMINE METABOLISM, MELANIN
FORMATION, AND SCLEROTIZATION OF THE CUTICLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anopheles stephensi (Indo-Pakistan malaria mosquito).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Probable 26S proteasome non-ATPase regulatory subunit 3 (26S
proteasome subunit 33) (Diphenol oxidase A2 component) (DOX-A2)
                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
InterPro; IPR000205; NAD_binding.
Oxidoreductase; NAD; Carotenoid biosynthesis; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 37; DB 1; Length 500; Pred. No. 80;
                                                                                                                                                                                                                                                   Length 500;
                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                          114 NAD (POTENTIAL).
56067 MW; 2E3721B87EE6CBC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    500 AA; 56840 MW; 4B98EA0F702EEB5C, CRC64;
                                                                                                 CHLOROPLAST (POTENTIAL)
                                                                                                                                 LYCOPENE BETA CYCLASE.
                                                                                                                                                                                                                                                   Score 37; DB 1;
Pred. No. 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           500 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20296811; PubMed=10835480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AJ250874; CAB61220.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                   45.7%;
72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.7%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000717; PCI.
Pfam; PF01399; PCI; 1.
SMART; SM00088; PINT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                            Local Similarity 72.
                                                                                                                                                                                                                                                                                                                                                                                                                                   372 TLAAAPVVANA 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                           9 TAAXAPVVXNA 19
                                                                                                 81
500
                                         Oxidoreductase; NAD;
Transit peptide.
TRANSIT
                                                                                                                                                                                       500 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI TaxID=30069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOXA2 OR DOX-A2.
```

```
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUC1 XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                005049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 30
MUC1_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                         Thielen J.;
Thesis (1993), Heinrich-Heine University / Duesseldorf, Germany.
-!- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid + NADH.
-!- PATHWAY: Ethanol utilization; second step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                       01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Aldehyde dehydrogenase 2, mitochondrial precursor (EC 1.2.1.3)
                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Mitochondrial matrix (Potential). -!- SIMILARITY: Belongs to the aldehyde dehydrogenase family. -!- CAUTION: IS NOT PRESENT IN YEAST GENOME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALDEHYDE DEHYDROGENASE 2.
NAD (ADP PART) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.7%; Score 37; DB 1; Length 511; llarity 44.4%; Pred. No. 82; Conservative 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ( SIMILARITY.
( SIMILARITY.
70EDAE951B84EE4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterFro; LEASTON 1.
PEAM; PF00171; aldedh; 1.
PROSITE; PS00070; ALDEHYDE DEHYDR_GLU; 1.
PROSITE; PS00687; ALDEHYDE DEHYDR_GLU; 1.
Oxidoreductase; NAD; Mitochondrion; Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              William, 1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein C30D11.14c in chromosome I.
SchZ30D11.14C.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           534 AA
                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S31308; S31308.
HSSP; POS5091; 1CW3.
1GD5; LO000075; ALD2.
INTERPRO; IPR002086; Aldehyde_dehydr.
                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        331 331 E
511 AA; 56466 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z17314; CAA78962.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
              5 TPLTTAAXAPVV 16
                                      7 TPTATAASEPIV 18
                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      511
279
297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Local 8; Conserve
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                     NCBI_TaxID=4932;
                                                                                                                                                                       ALD2 OR ALDH2.
                                                                                                DHAY YEAST
P32872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YAJE SCHPO
Q09911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NP BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YAJE SCHPO
                                                                                        (EAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 29
                                                                                                   OS GERTA SO
```

```
MEDLINE-1848401; Pubmed-allabases

RA MEDLINE-1848401; Pubmed-allabases

RA Squuros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA Squuros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

RA Gentles S., Goble A., Hamlin N., Harris D., Hiddlyo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarch S., Huckle E.J., Hunt S., Jagels K.,

A James K., Jones M., Leather S., McDonald S., McLean J.,

RA Holroyd S., Hornsby T., Bearson D., Quail M.A., Rabbinowitsch E.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Rutherford J., Simmonds M., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

Weltjens I., Vonckaart G., Aert R., Robben J., Grymonprez B.,

Weltjens I., Vonckaart G., Aert R., Robben J., Grymonprez B.,

RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

Goffeau A., Cadieu B., Dreano S., Gloux S., Lelaure V., Mottier S.,

Goffeau A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

RA Boaga R.R., Cruzado L., Jimenez J., Sanchez M.,

Baga R.R., Cruzado L., Jimenez J., Sanchez M.,

RA Cerrutti L., Lowe T., Moreno S., Armstrong J., Forsburg S.L.,

"The genome sequence of Schizoaaccharomyces pombe.";

"The genome sequence of Schizoaaccharomyces pombe.";

"The genome sequence of Schizoaaccharomyces pombe.";

"The genome sequence of Schizoaaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0cT-1994 (Rel. 30, Created)
01-0cT-1994 (Rel. 30, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
11 thegumentary mucin C.1 (FIM-C.1) (Fragment).
12 Xenopus laevis (African clawed frog).
13 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.7%; Score 37; DB 1; Length 534; 53.3%; Pred. No. 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Geneba Spombe, SPAC30D11.14c; -.
Geneba Spombe, SPAC30D11.14c; -.
InterPro, IPR004087; KH dom.
SMART; SM00322; KH; 1.
Hypothetical protein.
SEQUENCE 534 Aa; 59035 MW; B38F20B8A20A47F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        662 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                               MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z67961; CAA91900.1; -. PIR; T38585; S62572.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         415 OEKTOPTNASPAPLV 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                          SEQUENCE FROM N.A.
NCBI_TaxID=4896;
```

```
BY SIMILARITY.
BY SIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Campylobacter jejuni.
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales;
Campylobacteraceae, Campylobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
.
12 X APPROXIMATE TANDEM REPEATS, THR-
RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isoform 5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Missing (In isoform 4 and isoform /FTId=VSP_004647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /FTId=VSP 004647.
Missing (in isoform 4 and is FTId=VSP 004648.
Missing (in isoform 5).
/FTId=VSP 004649.
Missing (in isoform 2 and is /FTId=VSP 004659.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 T -> A.
67774 MW; F085277F1ED2FD40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /FTId=VSP 004650.
Missing (in isoform 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 1; 1
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'FTId=VSP_004651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                   3-11.
3-12.
P-TYPE 4
P-TYPE 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FTSK CAMJE STANDARD; PRT; Q46089; Q9PP45; 01-NOV-1997 (Rel. 35, Created) 16-OCT-2001 (Rel. 40, Last sequence 15-SEP-2003 (Rel. 42, Last annotation Cell division protein firsk homolog. FTSQ OR CJ0886C.
                                 3-1.
3-2.
3-2.
3-5.
3-6.
3-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 KTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 КАРТТАААТАРТТААА 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Conservative
                                 276
354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      662 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     420
                                                                                                                                                                                                                                                                                                                     82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      354
                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /ARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /ARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
                                                                                 REPEAT
REPEAT
                                                                                                                  REPEAT
REPEAT
                                                                                                                                                                                                   REPEAT
REPEAT
DOMAIN
                                 REPEAT
                                                 REPEAT
                                                                  REPEAT
                                                                                                                                                   REPEAT
                                                                                                                                                                   REPEAT
                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 31
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COSSEPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1-8.
B TYPE 1.
R X APPROXIMATE TANDEM REPEATS, THR-RICH.
2-1.
                                        Hauser F., Hoffmann W.;

"P-domains as shuffled cysteine-rich modules in integumentary mucin [P-domains as shuffled cysteine-rich modules in integumentary mucin [C.1] (FIM-C.1) from Xenopus laevis. Polydispersity and genetic polymorphism.";

J. Biol. Chem. 267:24620-24624(1992).

-!-FUNCTION: Could be involved in defense against microbial infections. Protects the epithelia from external environment.

-!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=7;

Comment=Additional isoforms seem to exist. Experimental confirmation may be lacking for some isoforms;
                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q05049-5; Sequence=VSP_004646, VSP_004649, VSP_004650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 X 8 AA APPROXIMATE TANDEM REPEATS,
ALA/THR-RICH.
                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q05049-4; Sequence=VSP_004647, VSP_004648;
                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=205049-6; Sequence=VSP_004646, VSP_004648;
SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6 AND 7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: Contains 6 P-type (trefoil) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat, Glycoprotein; PIREFOIL; 6.
NON_TER 1 1
DOWAIN 81 111
                                                                                                                                                                                                                                                                                                      IsoId=Q05049-2; Sequence=VSP_004650;
                                                                                                                                                                                                                                                                                                                     Name=3;
IsoId=Q05049-3; Sequence=VSP_004651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=205049-7; Sequence=VSP_004647;
                                                                                                                                                                                                                                                   Name=1;
IsoId=Q05049-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ۶. w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-TYPE
P-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: SKIN. PTM: EXTENSIVELY O-GLYCOSYLATED.
              TISSUE=Skin;
MEDLINE=93077556; PubMed=1447205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A45155; A45155.
HSSP; P01359; ZPSP.
InterPro; IPR000519; P_trefoil.
Pfam; PF000088; trefoil; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0680; PTREFOIL.
SMART; SM00018; PD; 6.
PROSITE; PS00025; P_TREFOIL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L02115; AAA74725.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
```

ô

```
607 KSPLTIALGKDIVGNA 622
                                                                                                                                                                                                                                                                                                                                                                                                Flaveria anomala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rissum=Leaf;
                                                                                                                                        FLAAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Flaveria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                   SOUTH THE WARRANT AND THE SOUTH THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                            STRAIN=NCTC 11168;
MEDLINE=20150912; PubMed=10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni
reveals hypervariable sequences.";
                                                                                                        MEDLINE=94341566; PubMed=8063102;
Miller S., Pesci E.C., Pickett C.L.;
"Generic organization of the region upstream from the Campylobacter
jejuni flagellar gene flhA.";
Gene 146:31-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TARLER DESCRIPTION | Integral membrane protein (Potential).
-!- SUBCELLULAR LOCATION: I FLSK/SpoIIIE domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interpro; IPR002543; PtsK SpollIB.
Pfam, PP01580; PtsK SpolIIE.
PROSITE; PS50901; FTSK SPOIIE.
Cell division; ATP-binding; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAYAIFST -> IVYGFFSI (IN REF. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.7%; Score 37; DB 1; Length 946
50.0%; Pred. No. 1.5e+02;
Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> V (IN REF. 1).
-> E (IN REF. 1).
-> V (IN REF. 1).
825D15A43BEAB4FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T -> K (IN REF. 1).
IGF -> FSL (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S -> T (IN REF. 1).
A -> S (IN REF. 1).
PNS -> REF (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IN REF. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RN -> KK (IN REF. 1).
LA -> IE (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REF. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> A (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A -> G (IN REF. 1)
FLF -> SLL (IN REF
V -> L (IN REF. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H -> R (IN REF. 1)
S -> Y (IN REF. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FTSK/SPOILIE.
ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EN -- VF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U06951; AAA61512.1; ALT_INIT.
EMBL; AL139076; CAB73144.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107862 MW;
                                                                                       STRAIN=ATCC 55026 / 81-176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50...
Best Local Similarity 50...
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 403:665-668(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; F81361; F81361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      735
888
946 AA;
                                                             SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
        NCBI_TaxID=197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NP_BIND
TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
CON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRANSMEN
```

```
Nam Q., Bauwe H.;
Nam Q., Bauwe H.;
Nam Q., Bauwe H.;
The GDCSP gene encoding P-protein of the glycine cleavage system in the GDCSP gene encoding Plaveria anomala.";
The GDCSP gene Register PGR99-004.

(In) Plant Gene Register PGR99-004.

(In) Plant Gene Register possible to glycine cleavage system catalyzes the degradation of glycine. The P protein binds the alpha-amino group of glycine through its pyridoxal phosphate cofactor, CO(2) is released and the remaining methylamine moiety is then transferred to the lipoamide cofactor of the H protein.

(In) Inpommide cofactor of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; campanulids; Asterales; Asteraceae; Asteroideae; Tageteae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 1034 GLYCINE DEHYDROGENASE [DECARBOXYLATING] 770 770 PYRIDOXAL PHOSPHATE (BY SIMILARITY). 1034 AA; 112695 MW; C2F424C76EF104BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oxidoreductase; Mitochondrion; Pyridoxal phosphate; Transit peptide.
TRANSIT 1 63 MITOCHONDRION (POTENTIAL).
                                                                                               15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Glycine dehydrogenase (decarboxylating), mitochondrial precursor (EC 1.4.4.2) (Glycine decarboxylase) (Glycine cleavage system P-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37; DB 1; Lengtn 100 Pred, No. 1.78+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MITOCHONDRION (POTENTIAL)
GLYCINE DEHYDROGENASE [DE
PRT; 1034 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSK5 HUMAN STANDARD; PRT; 1064 AA Q9NQ38; 075770; 096PP2; 096PP3; 16-CCT-2001 (Rel. 40, Created) L16-CCT-2001 (Rel. 40, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                     15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last seq
15-SEP-2003 (Rel. 42, Last ann
Glycine dehydrogenase [decarbo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF02347; GDC-P; 1.
TIGRFAMB; TIGR00461; gcvP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z99762; CAB16911.1; -
InterPro; IPR003437; GDC-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           811 EESOPLGTIAAAP 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 EEKTPLTTAAXAP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
es 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=35877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISKS HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPE
```

ö

Gaps

.. 0

Length 946;

```
PEPTIDE
PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                        EMBL;
EMBL;
EMBL;
                                                                                                                                            EMBL;
EMBL;
                                                                                                                                                                      EMBL;
EMBL;
                                                                                                                                                                                                EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                       EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                           EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                             EMBL;
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE THYMUS. ALSO FOUND IN THE ORAL MUCOSA, PARATHYROID GLAND, BARTHOLIN'S GLANDS, TONSILS, AND VACINAL EPITHELIUM. VERY LOW LEVELS ARE DETECTED IN LUNG, KIDNEY, AND PROSTATE.

DOMAIN: CONTAINS AT LEAST ONE ACTIVE INHIBITORY DOMAIN FOR TRYPSIN (DOMAIN 6)
                                                                                                                                           TISSUE=Epithelium;
MEDLINE=99348267; PubMed=10419450;
Maegert H.-J., Staendker L., Kreutzmann P., Zucht H.-D., Reinecke M.,
Sommerhoff C.P., Fritz H., Forsemann M.-G.;
"LEKII, a novel 15-domain type of human serine proteinase inhibitor.";
J. Biol. Chem. 274:21499-21502(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The spectrum of pathogenic mutations in SPINK5 in 19 families with Netherton syndrome: implications for mutation detection and first case of prenatal diagnosis."; Invest. Dermatcol. 117:179-187(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISEASE: Defects in SPINKS are the cause of Netherton syndrome (NS) [MINI-256300], a severe autosomal recessive disorder. It is characterized by congenital ichthyosis with defective confication, a specific hair shaft defect known as trichorrexis invaginate or "bamboo hair", atopic dermatitis, and hayfever. High post-natal mortality is due to failure to thrive, infections and hypernatraemic dehydration.
           Serine protease inhibitor Kazal-type 5 precursor (Lympho-epithelial Kazal-type related inhibitor) (LEKTI) [Contains: Hemofiltrate peptide HF6478; Hemofiltrate peptide HF7665].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of proteins from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Walley A.J., Chavanas S., Moffatt M.F., Esnouf R.M., Ubhi B.,
Lawtence R., Wong K., Abecasis G.R., Jones B.Y., Harper J.I.,
Havnanian A., Cookson W.O.C.M.;
"Gene polymorphism in Netherton and common atopic disease.";
Nat. Genet. 29:177-178(2001)
-i- FUNCTION: SERINE PROFEASE INHIBITOR, PROBABLY IMPORTANT FOR THE
ANTI-INPLAMMATORY AND/OR ANTIMICROBIAL PROTECTION OF MUCOUS
                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21403066; PubMed=11511292;
Sprecher E., Chavanas S., DiGlovanna J.J., Amin S., Nielsen K., Frendiville J.S., Silverman R., Esterly N.B., Spraker M.K., Guelig de Luna M.L., Williams M.L., Buehler B., Siegfried B.C., Van Maldergem L., Pfendner E., Bale S.J., Uitto J., Hovnanian A.,
                                                                                                                                                                                                                                              MEDLINE=20296612; PubMed=10835624; Chavanas S., Bodemer C., Rochat A., Hamel-Teillac D., Ali M., Livine A.D., Bonafe J.-L., Wilkinson J., Taieb A., Barrandon Y., Harper J.I., de Prost Y., Hovnanian A.; Mutations in SPINKS, encoding a serine protease inhibitor, cause Netherton syndrome.";
                                                                             Euteleostomi;
                                                           Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND VARIANT GLU-420.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Contains 15 Kazal-like domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Foreskin keratinocyte;
MEDLINE=21477652; PubMed=11594460;
Ahmed A., Kandola P., Ziada G., Parenteau N.;
"Purification and partial amino acid sequence epidermal keratinocyte conditioned medium.";
J. Protein Chem. 20:273-278(2001).
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 202-222 AND 266-294 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPITHELIA.
SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                Nat. Genet. 25:141-142(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 490-507.
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT GLU-420.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Richard G.;
                                                    SPINKS
```

```
between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005576; C:extracellular; NAS.
GO; GO:0004867; F:serine protease inhibitor activity; NAS.
GO; GO:0004867; F:serine protease inhibitor activity; NAS.
GO; GO:0005960; P:anti-inflammatory response; NAS.
InterPro; IPR002350; kazal.
InterPro; IPR00505; kazal; 7.
SMART; SM00280; KAZAL; 14.
PROSITE; PS00282; KAZAL; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ď.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SERINE PROTEASE INHIBITOR KAZAL-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEPTIDE HF6478
PEPTIDE HF7665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serine protease inhibitor; Repeat; Signal; Polymorphism.
SIGNAL 1 22 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ATYPICAL)
(ATYPICAL)
(ATYPICAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ATYPICAL)
(ATYPICAL)
(ATYPICAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ATYPICAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ATYPICAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ATYPICAL) (ATYPICAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ATYPICAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KAZAL-LIKE 1 (A
KAZAL-LIKE 2 (A
KAZAL-LIKE 4 (A
KAZAL-LIKE 5 (A
KAZAL-LIKE 6 (A
KAZAL-LIKE 6 (A
KAZAL-LIKE 9 (A
KAZAL-LIKE 9 (A
KAZAL-LIKE 10 (
KAZAL-LIKE 11 (
KAZAL-LIKE 11 (
KAZAL-LIKE 12 (
KAZAL-LIKE 12 (
KAZAL-LIKE 13 (
KAZAL-LIKE 13 (
KAZAL-LIKE 13 (
KAZAL-LIKE 13 (
KAZAL-LIKE 14 (
KAZAL-LIKE 14 (
KAZAL-LIKE 15 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HEMOFILTRATE
HEMOFILTRATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOINED.
JOINED.
JOINED.
                                                                                                                                                                   JOINED.
JOINED.
JOINED.
JOINED.
JOINED.
JOINED.
JOINED.
JOINED.
                                                                                                                                                                                                                                                                                                                     JOINED.
JOINED.
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                JOINED.
JOINED.
JOINED.
JOINED.
                                                                                                                                                                                                                                                                                       JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOINED
                                                                                                          EMBL; AJ228139; CAB40839.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AJ391251, CAB96877.1, JUNE BMBL, AJ391252, CAB96877.1, JUNE BMBL, AJ391253, CAB96877.1, JUNE BMBL, AJ391254, CAB96877.1, JUNE BMBL, AJ391254, CAB96877.1, JUNE BMBL, AP295784, AAK97139.1, EMBL, AP295784, AAK97139.1, EMBL, AP295783, AAK97140.1, SMSL, BJ109, 1PCB.

MIM, 605010,
                                                                                                                                                                    CAB96877.1;
                                                                                                                                                     CAB96877.1;
                                                                                                                                                                                                  CAB96877.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                             CAB96877.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAB96877.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAB96877.1;
                                                                                                                                                                                  CAB96877.1;
                                                                                                                                                                                                                CAB96877.1;
                                                                                                                                                                                                                                                                                                                                                                                                              CAB96877.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAB96877.1;
                                                                                                                                                                                                                                CAB96877.1
                                                                                                                                                                                                                                                                                                                                                                                                                               CAB96877.1
                                                                                                                                                                                                                                                              CAB96877.1
                                                                                                                                                                                                                                                                                                        CAB96877.1
                                                                                                                                                                                                                                                                                                                        CAB96877.1
                                                                                                                                                                                                                                                                                                                                       CAB96877.1
                                                                                                                                                                                                                                                                                                                                                    CAB96877.1
                                                                                                                                                                                                                                                                                                                                                                    CAB96877.1
                                                                                                                                                                                                                                                                                                                                                                                   CAB96877.1
                                                                                                                                                                                                                                                                                                                                                                                                 CAB96877.1
                                                                                                                                                                                                                                              CAB96877.
                                                                                                                                                                                                                                                                                          CAB96877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1064
423
423
1151
1151
2214
2214
4211
473
556
681
681
757
757
903
903
                                                                                                                        AJ391230; (AJ270944; (AJ391231; (
                                                                                                                                                                                                AJ391234;
AJ391235;
                                                                                                                                                                    AJ391232;
AJ391233;
                                                                                                                                                                                                                                                                                                                                                                                                                              AJ391246;
AJ391247;
AJ391248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AJ391249;
AJ391250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23
356
356
288
288
223
223
239
4435
494
                                                                                                                                                                                                                                 AJ276579;
                                                                                                                                                                                                                                              AJ391236;
                                                                                                                                                                                                                                                              AJ276580;
                                                                                                                                                                                                                                                                                          AJ391238;
                                                                                                                                                                                                                                                                                                                        AJ391240;
                                                                                                                                                                                                                                                                                                                                       AJ391241;
                                                                                                                                                                                                                                                                                                                                                                    AJ391242;
                                                                                                                                                                                                                                                                                                                                                                                  AJ391243;
                                                                                                                                                                                                                                                                                                                                                                                                   AJ391244;
                                                                                                                                                                                                                                                                                                                                                                                                                AJ391245;
                                                                                                                                                                                                                                                                                                                                                      AJ276578
                                                                                                                                                                                                                                                                                                      AJ39123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM; 256500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
DISULFID
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 24, Last sequence update)
Genome polyprotein [Contains: Capsid protein C (Core protein); Matrix protein (Envelope glycoprotein M); Major envelope protein); Matrix protein (Envelope glycoprotein M); Major envelope protein); Monstructural proteins NS1, NS2, NS4A and NS4B; Protease/helicase (EC 2.7.7.48)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Virology 176:643-647(1990)

-!- CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the viral precursor polyprotein, commonly with Asp or Glu in the P6 position, Cys or Thr in P1 and Ser or Ala in P1'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       {RNA}(N).
SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MRNA.
OCTAPEPTIDE A-G-Y-G-S-T-L-T, FURTHER ON A 16-RESIDUE AND A REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
MISCELLARBOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE. SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Osatomi K., Sumiyoshi H.; "Complete nucleotide sequence of dengue type 3 virus genome RNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    position, Cys or Thr in P1 and Ser or Ala in P1'. CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1567;
                                                                                                                                                                                                                                                                                                          HSSP; P06620; 11NA.
InterPro; IRRO0258; Ice_nucleatn.
Pfam; PF00818; Ice_nucleation; 81.
PRINTS; PR00327; ICENUCLEATN.
PROSITE; PS00314; ICE NUCLEATION, 57.
SECONTE; PS00314; ICE NUCLEATION; 57.
SEQUENCE \ 15567 AA; 152548 MW; C8B451D959ECAD63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37; DB 1; I
Pred. No. 2.6e+02;
1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 3390 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90266483; PubMed=2345967;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.7%;
58.3%;
                                                                                                                                                                                                                                                                                      EMBL; X52970; CAA37140.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 EATPVATVAAAP 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 EKTPLTTAAXAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dengue virus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=11069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Flavivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLG DEN3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NS5)]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLG_DEN3
                                                                                 <u>;</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xanthomonas campestris pv. translucens ";
Mol. Gen. Genet. 223:163-166(1990).
-!- FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUCLEATE
CRYSTALLIZATION IN SUPERCOOLED WATER.
-!- SUBCELLULAR LOCATION: Outer membrane (By similarity).
-!- SUBCELLULAR LOCATION: Outer membrane (By similarity).
-!- DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2CEKDSLS<sup>-</sup> - DAASKNEDQ (IN REF. 1).
-> V (IN REF. 1).
-> Q (IN REF. 1).
4418063DEABC341C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xanthomonas campestris (pv. translucens).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Conserved repetition in the ice nucleation gene inaX from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 37; DB 1; Length Luc
Pred. No. 1.7e+02;
5; Indels
                                                                                                                                                                                                                                BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VAR 015537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1567 AA.
                       SIMILARITY
SIMILARITY
SIMILARITY
SIMILARITY
SIMILARITY
SIMILARITY
SIMILARITY
SIMILARITY
SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GOCEKDSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91080859; PubMed=2259339;
           .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xanthomonadaceae; Xanthomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.7%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESSTPGTTAASMP 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EEKTPLTTAAXAP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ice nucleation protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1028
1025
1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhao J., Orser C.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Best Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1064 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                        225
239
297
311
367
381
                                                                                                                                                                                                                                    437
451
496
510
567
581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=X56S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ICEN XANCT P18127;
                                                                                                                                                                             DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                            DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1048
                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INAX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ICEN XANCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 34
```

셤

ö

Gaps

;

```
(POTENTIAL)
                                                                   Length 3390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U66405; AA4848388.1; -
EMBL; 281122; CAB03359.1; -
PIR, T24882; T24882.

R wormPep; T13F2.8; CE13633.

R interPro, IPR001612; Caveolin.

P fan; PF01146; Caveolin; 1.
PROSITE; PS01210; CAVEOLIN; FALSE_NEG.

Transmembrane; Lipoprotein; Palmitate.

(W Transmembrane; Lipoprotein; Palmitate.
        N-LINKED (GLCNAC. ..) (POTF
N-LINKED (GLCNAC. ..) (POTF
N-LINKED (GLCNAC. ..) (POTF
N-LINKED (GLCNAC. ..) (POTF
M-LINKED (GLCNAC. ..) (POTF
M-, 666E8F70F1E1756E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
PALMITATE (POTENTIAL).
, F07B12DEB4D6F13A CRC64;
                                                                    Score 37; DB 1; 1
Pred. No. 5.7e+02;
 (GLCNAC
                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26291 MW;
                                                                    45.7%;
                                                378057
                                                                               53.8%;
                                                                                                                        3315 EDKTPVTTWEDVP 3327
                                                                                                            2 EEKTPLTTAAXAP 14
                                                                              Local Similarity 53.8
les 7; Conservative
                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                    Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235
         2304
2456
2702
2712
                                                3390 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235 AA;
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Bristol N2;
                                                                                                                                                                                                                                           CAV-1 OR T13F2.8.
2300
2304
2456
2702
                                                                                                                                                                                  CAEEL
                                                                                                                                                                                                                                 Caveolin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIPID
          CARBOHYD
CARBOHYD
                            CARBOHYD
                                        CARBOHYD
                                                SEQUENCE
                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                         094051
                                                                                        Matches
FFFFFS
                                                                                                                               g
                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NONSTRUCTURAL PROTEIN NS4A.
NONSTRUCTURAL PROTEIN NS4B.
NNA-DIRECTED RNA POLYMERASE (NS5)
ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                      MAJOR ENVELOPE PROTEIN E.
NONSTRUCTURAL PROTEIN NS1.
NONSTRUCTURAL PROTEIN NS2A.
NONSTRUCTURAL PROTEIN NS2B.
PROTEASE/HELICASE (NS3).
                                                                                                                                                                                                                                                                                                                                                                                                                             ENVELOPE GLYCOPROTEIN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
POTENTIAL.
5 (POTENTIAL).
BY SIMILARITY.
N-LINKED (GLCN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEAH BOX.
POTENTIAL.
POTENTIAL.
                                              Plavi glycoprote.
Flavi helicase.
Flavi M.
Flavi MS1.
Flavi NS2A.
Flavi NS2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                   ProDom; PD001556; Flavi glycoprotE; 1.
ProDom; PD001496; Flavi NS1; 1.
                                                                                                                                                            PR001650; Helicase C.
PR007095; RNA pol DS PS.
PR007094; RNA pol PSvir.
03; Flavi_capsid; 1.
                                                                                                          PR000404; Flavi NS4A.
PR001528; Flavi NS4B.
PR000208; Flavi NS5.
PR002535; Flavi propep.
                                                                                                                                                                                                 Flavi_glycop_C; 1.
Flavi_glycoprot; 1.
Flavi_helicase; 1.
                                                                                                                                                                                                                                                                                                        Flavi_propep; 1
                                                                                                                                                                                                                                                     Flavi_NS2A; 1.
Flavi_NS2B; 1.
Flavi_NS4A; 1.
Flavi_NS4B; 1.
                                                                                                                                                                                                                                                                                                                           Pfam; PF00271; helicase_C; 1.
                                                                                                                                                                                                                                                                                   PF01349; Flavi_NS4B; 1. PF00972; Flavi_NS5; 1.
                            interPro; IPR001410; DEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                       773
1184
11343
11473
2092
2378
2490
3390
                                                                                                                                                              InterPro; IPR001650;
                                                                                                  InterPro; IPR000487;
                                                                                                                      InterPro;
                                                                                                                                                                       InterPro;
                                                                                                                                                                                  InterPro;
                                                                                                                                                   InterPro;
                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
CHAIN
CHAIN
CHAIN
CHAIN
NP BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
PROPEP
CHAIN
                                                                                                                                                                                                                                                                                                       Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
CHAIN
CHAIN.
                                                                                                                                                                                                                                                               Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                   Pfam;
                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                           Pfam;
                                                                                                                                                                                                                                                      Pfam;
                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                 Pfam;
```

DONARA CON CONTRACTO CONTR

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Bristol N2;
MEDLINE=97153022; PubMed=8999956;
Tang Z., Okamoto T., Boontrakulpoontawee P., Katada T., Otsuka A.J.,
Lisanti M.P.;
"Identification, sequence, and expression of an invertebrate caveolin
gene family from the nematode Caenorhabditis elegans. Implications.
for the molecular evolution of mammalian caveolin genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL) . (POTENTIAL) . (POTENTIAL) .
```

```
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR, S04261, ATBPP1.
InterPro, IPR005039; Anti_rep.
Pfam, PF03374; ANT; 1.
DNA-binding.
                                                                             Bacteria, Proteobacteria, Gam
Enterobacteriaceae, Serratia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.4%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X15639; CAA33659.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X78412; CAA55176.1; -. PIR; S47098; S47098.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 53.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 EEKTPLTTAAXAP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 ОНКТРАКТААКР 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                       DamX protein (Fragment)
  01-OCT-1996 (Rel. 34,
                                                            Serratia marcescens
                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PI-like viruses.
NCBI_TaxID=10678;
                                                                                                                     NCBI_TaxID=615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hansen E.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANT BPP1
P19655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MARKARA MARKAR
  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        There are no restrictions on its ng as its content is in no way wed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i - FUNCTION: GAP CLASS SEGMENTATION PROTEIN THAT CONTROLS DEVELOPMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OF HEAD STRUCTURES (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: BELONGS TO THE HUNCHBACK FAMILY OF C2H2-TYPE ZINC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baker R.H., Desalle R.; "Multiple sources of character information and the phylogeny of Hawaiian Drosophilids.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                               ;
                                                                                                                                                                                                                                                                                                                                                               Drosophila mimica (Fruit fly) (Idiomyia mimica).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Booptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                       DB 1; Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.4%; Score 36; DB 1; Length 158; 50.0%; Pred. No. 37; ive 1; Mismatches 7; Indels
                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158
17576 MW; 114B650BD4DC8CDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FlyBase, FBgn0023764, Dmic\hb.
Developmental protein, Gap protein, Zinc-finger,
Metal-binding, DNA-binding, Repeat, Nuclear protein.
                                                                                                                                                                                                                                                                  046248; 046249;
16-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed.
                                                                                                                                                                                                                                               158 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 32, Created)
(Rel. 32, Last sequence update)
                                                            1; Mismatches
                       45.1%; Score 36.5; 62.5%; Pred. No. 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-THR.
POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLY-HIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-GLN
                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                Hunchback protein (Fragments).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RTTTTTAAAAPTTTAA 105
                                                                                                                                    10 EEOIPLTYAAVAAPTV 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 KTPLTTAAXAPVVXNA 19
                                                                                                       2 EEKTPLITAA-XAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol. 46:654-673 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U93012; AAC03260.1; -.
                                          Best Local Similarity 62.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U93013; AAC03261.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FINGER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 38
DAMX SERMA
ID DAMX SERMA
                                                                                                                                                                                                                                                 HUNB DROMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90
                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P454<u>5</u>9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                      DA LI
                                                                                                         ò
                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antirepressor protein 1 (ANT1) (Repressor bypass protein B) (REBB) (Contains: Antirepressor protein 2 (ANT2) (Repressor bypass protein A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                  Wackernagel W.;
                                                                                                                                                                                                                                                                                                         -!- FUNCTION: DIRECTLY OR INDIRECTLY INTERFERES WITH CELL DIVISION
Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Structure and regulation of the lytic replicon of phage Pl."; J. Mol. Biol. 207:135-149(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteriophage P1.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Indels
                                                                                                                                                                                              STRAIN=Sr41;
Ostendorf T., Cherepanov P., Jekel M., de Vries J., Wack
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 AA; 22157 MW; 3D1BDD43F8D6C401 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB 1;
Pred. No. 50;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                322 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=89293847; PubMed=2661831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last seq
28-FEB-2003 (Rel. 41, Last ann
```

```
Mood V., Gwilliam R., Rajandram M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gontles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgeon G., Horbyds S., Hornsby T., Huckarls E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Lather S., McDonald S., McLean J., Andrew D., Oneil S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Sauros M., Seager K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor K., Taylor K., Walb M., Rabinowitsch E., Androfor M., Simmonds M., Squares S., Stevens K., Taylor K., Taylor K., Walb M., Mushim M., Miltehead S., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., A. Berz M., Cadieu E., Dreans S., Gloux S., Lelarach E., Pohl T.M., Berr M., Cadieu E., Dreans S., Gloux S., Lelarach W., Garzon A., Thode G., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Dominguez A., Revuelta J.L., Mocreno S., Armstrong J., Forsburg S.L., Sanchez M., del Rey F., Benito J., Sanchez M., del Rey F
                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ohi M.D., Link A.J., Ren L., Jennings J.L., McDonald W.H., Gould K.L.; "Protecomics analysis reveals stable multiprotein complexes in both fission and budding yeasts containing Myb-related Cdc5p/Ceflp, novel pre-mRNA splicing factors, and BNRAS."; Mol. Cell. Biol. 22:2011-2024(2002).

-!- FUNCTION: Involved in mRNA splicing where it associates with cdc5 and the other cwf proteins as part of the spliceosome.
                                                                                                                                                                           Gaps
                                                                                                                                                                              ô
                                                                                                                         44.4%; Score 36; DB 1; Length 322;
46.7%; Pred. No. 76;
Live 3; Mismatches 5; Indels
1 322 REBB PROTEIN.
84 322 REBA PROTEIN (POTENTIAL).
258 277 H-T-H MOTIF (POTENTIAL).
322 AA; 35994 MW, 80981CE2AA7A851A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEE-2003 (Rel. 41, Created)
28-FEE-2003 (Rel. 41, Last sequence update)
28-FEE-2003 (Rel. 41, Last annotation update)
CWF17 OR SPBC1289.11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBUNIT: Interacts with cdc5.
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- SIMILARITY: Contains 7 WD repeats.
                                                                                                                                                                                                                                                                                                                                                                                                            340 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21881936; PubMed=11884590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=972;
MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                           |: |:|:| || |
92 EKTAPVTSATPAPAV 106
                                                                                                                                                                                                                              2 EEKTPLTTAAXAPVV 16
                                                                                                                    Query Match
Best Local Similarity 46.7°
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DENTIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                         SCHPO
                                               DNA BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                 094620;
                                                                                                                                                                                                                                                                                                                                                       RESULT 40
CWFH_SCHPO
                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                 FT
                                                                                                                                                                                                                                ઠે
```

```
the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                       Nuclear protein; mRNA processing; mRNA splicing; Repeat; WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
                                                                                                                                                                                                                                                                                                                                                                                                                        44.4%; Score 36; DB 1; Length 340; 66.7%; Pred. No. 80;
                                                                                                                                                                                                                                                                                                                                                                                             BBAA5938CA4C24C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                         SMART; SM00320; WD40; 7.
PROSITE; PS00678; WD REPEATS_1; 2.
PROSITE; PS50002; WD REPEATS_2; 7.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                      WD 2.
WD 3.
WD 4.
WD 5.
                                                                                                                            FILM, 123924; 123924.

GeneDB SPonde; SPBC1289.11; -.

InterPro; IPR001680; WD40.

Pfam; PF00400; WJ40; 7.

PRINTS; PR00320; GPROTEINBRPT.

PRODOM; PD000018; WD40; 2.
                                                                                                                                                                                                                                                                                                                                                                                             340 AA; 37427 MW;
                                                                                                    EMBL; AL035675; CAB38691.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conservative
                                                                                                                      T39362; T39362
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
```

Search completed: January 28, 2004, 13:08:34 Job time : 12 secs

EEKYPLTAVAIA 186

2 EEKTPLTTAAXA 13

8 8

DIAGO, MARGIN SINI

Q89946 xanthomonas Q89069 xanthomonas Q89784 aeropyrum p Q875m9 listeria mo Q811a1 drosophila Q9440 caulobacter Q9440 caulobacter Q9465 human immun Q95018 halocynthia Q94018 drosophila Q8mlp2 drosophila Q80961 mus musculu Q02006 drosophila Q03462 zea mays (m Q94596 drosophila

Q8np51 corynebacte Q91gm5 oryza sativ Q8p4v3 xanthomonas

Q8b8m6 human adeno

OSmt63 drosophila OSm193 drosophila O9u3e3 caenorhabdi O9u4y3 ceratitis c

Q8p7w8 xanthomonas Q8zzx0 pyrobaculum

Q9se04 oryza sativ Q54272 streptomyce

Sequence:

Run on:

Searched:

Database

```
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales; Porphyromonadaceae; Porphyromonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=VPB3492;
Nakayama K., Sato K.;
Natalase.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AB083039; BAC20190.1; -.
SEQUENCE 485 AA, 55610 MW; 6D35EC7A7E59F8AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 50; DB 2;
Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   485 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                    Q8MT63
Q8ML93
Q9U3E3
Q9U4Y3
Q8PQ46
Q8PD69
Q9Y984
            Q54272
Q8P7W8
Q8ZZX0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                       Q811A1
Q9A4B0
Q9RD97
Q9BLH5
Q9W180
Q8MLP2
O57577
Q8CGF1
                                                                                                                                                                                                                                                                                                                                        Q03462
Q9W596
                                                                                                                                                                                                                                                                                                                                                                                   Q8NP51
Q9LGM5
Q8P4V3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                    Q8B8M6
Q9SE04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.7%;
68.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 EKTPLTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 EKNKLTTAAGAPVADN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23,
23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2003 (TrEMBLrel. 23, Catalase (EC 1.11.1.6).
                                                                                                                                                                                                                                                                               13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 68.00
Loca 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                            846
1266
1360
1399
                                                                                                                                                                                                                                                                                                                                      405
209
233
255
286
                                                                                                  212
2338
2238
2238
2252
2258
367
4477
774
778
805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Porphyromonas gulae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        48.8
48.8
48.1
1.8
48.1
48.1
                                                                                                                                9 4
                                                                                                                                                                                                                                                    000
                                                                                                                                                                                                                                                                                               449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Catalase HP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2003
                                                                                                                                                                                                                                                                                                                                      444444444444444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8ZGS4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8GRA4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8ZGS4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1
Q8GRA4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
Q8ZGS4
ID Q8ZG
AC Q8ZG
DT 01-M
DT 01-M
DT 01-M
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08294 Persinia pe
08672 caenorhabdi
091914 actinobacil
0883945 salmonella
096119 escherichia
094400 arabidopsis
023188 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9rnu2 streptococc
Q9x6x8 streptococc
Q9ft45 arabidopsis
Q9rjk9 streptomyce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P77924 pseudomonas
Q9dwh8 rat cytomeg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28gra4 porphyromon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8kkh4 hyphomicrob
                                                                                             January 28, 2004, 13:05:59; Search time 34 Seconds (without alignments) 144.206 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                             830525
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                830525 segs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                  Listing first 45 summaries
                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QBZGS4
QPRC14
QPRC14
QPRCW5
QBFKR4
Q9AI19
Q9AQ0
Q23188
Q8KKR4
P7724
Q9WWB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9X6X8
Q9FT45
Q9RJK9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_phage:*
sp_plant:*
sp_rodent:*
sp_virus:*
sp_virus:*
sp_vortebrate:*
sp_unclassified:*
                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                        1 XEEKTPLTTAAXAPVVXNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_invertebrate:*
sp_mammal:*
sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_archea:*
sp_bacteria:*
sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                         US-09-359-426C-2
81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp_human:*
                                                                                                                                                                                                                                                                                                                                                                                                                               SPTREMBL 23:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 :: 14 :: 15 :: 16 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 17 :: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10:
                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                          Perfect score:
```

.. 0

Gaps

0

Result No.

```
Query Match
Best Local Similarity
                                                                [3]
SEQUENCE FROM N.A.
STRAIN=Brigtol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P42321; 1M85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=714;
                                                                                                                                       Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Y4Na]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09RG14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9RG14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
Q8XGW5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29RG14
  SOUR DE REAL PROPERTIES DE COURT DE COU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                    d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=KIMS / Biovar Mediaevalis;
MEDLINE=22137863; PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
                                                                                                                                                                             MEDLINE=21470413; PubMed=11586360; Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Parkhill J., Wren B.W., Thomson N.R., Churcher C., Mungall K.L., Prentice M.B., Sebalhia M., James K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Genome sequence of Yersinia pestis, the causative agent of plague."; Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                             Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 16; Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRODOS; CATALAGE.
PRODOM; PD000510; Catalase; 1.
PROSITE; PS00438; CATALASE.2; Complete proteome.
Oxidoreductase; Peroxidase; Complete proteome.
SEQUENCE 480 AA; 55023 MW; 27A72FBAF096347E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.3%; Score 48; DB 3 68.8%; Pred. No. 6.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Genome sequence of Yersinia pestis KIM.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Nematoda, Chromadore:
Rhabditidae, Peloderinae, Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1998 (TrEMBLrel. 08, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Bacteriol. 184:4601-4611(2002)
                                                                                                                                                            STRAIN=CO-92 / Biovar Orientalis;
KATA OR YPO1207 OR KATE OR Y2981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, La
01-MAR-2003 (TrEMBLrel. 23, La
Hypothetical 47.3 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ414147; CAC90045.1; -. EMBL; AE013900; AAM86532.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR002226; Catalase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 EKTPLTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 KKKGLTTAAGAPVVDN 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 68.8
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00199; catalase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H34I24.2.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P42321; 1M85.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6239;
                            ersinia pestis
                                                                                       NCBI TaxID=632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perry R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    076672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               076672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         076672
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Figurski D.H.;

"Direct Salection of IS903 Transposon Insertions by Use of a Broad-
"Direct Salection of Catalase-Deficient Mutants of
Actinobacillus actinomycetemcomitans.";
J. Bacteriol. 181:72599.

-!- FUNCTION: OCCURS IN ALMOST ALL ABROBICALLY RESPIRING ORGANISMS AND
SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                             ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae, Actinobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20042351; PubMed=10572134;
Thomson V.J., Bhattacharjee M.K., Fine D.H., Derbyshire K.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heme: Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase.
SEQUENCE 484 AA; 54961 MW; D0E523AB2557D8CB CRC64;
                                                                                                                                                                                                                                                                                                                                          Length 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
Latreille P., Wamsley P., O'Brien D.; "The sequence of C. elegans cosmid H34I24."; Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                           Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF078784; AAK18967.1; -. wormbep; H34124.2; CE26681. Hypothetical protein. SEQUENCE 458 AA, 47285 MW; 2AF5BC94EDA0C324 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
EMBL; AF162654; AAF17882.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
1-WAY-2003 (TrEMBLrel. 23, Last annotation update)
Catalase (EC 1.11.1.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Actinobacillus actinomycetemcomitans (Haemophilus
                                                                                                                                                                                                                                                                                                                                       Score 46; DB 5;
Pred. No. 13;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 45; DB 2;
Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   306 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 484 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
PRODOM; PD000510; Catalase; 1.
PROSITE; PS00437; CATALASE 1; 1.
PROSITE; PS00438; CATALASE 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002226; Catalase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                386 KTPLTSGSSARVINNA 401
                                                                                                                                                                                                                                                                                                                                       56.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                4 KTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEROXIDE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 56.2<sup>3</sup>
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 LTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 LTTAAGAPVVDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          actinomycetemcomitans)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8XGW5
```

```
MEDLINE=21101044; PubMed=11159989;
                    MEDLINE=22388234; PubMed=12471157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Infect. Immun. 69:937-948(2001).
EMBL; AF286671; AAK27331.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002173; PfkB.
InterPro; IPR002139; Ribokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 EKVPCTSSGVAPIFVNA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 EKVPCTSSGVAPIFVNA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 EKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 EKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                        54.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00990; RIBOKINASE
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 47.11.

Best Local Similarity 67.11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00294; pfkB; 1.
                                                                                                                                                                                                                                                                                                 306 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P05054; 1RK2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=AL862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isolates.";
                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9AI19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9A119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 094AQ0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
Q94AQ0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9AI19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIESES. Lyphi; STRAIN=CT18;
MEDLINE=21534947; PubMed=11677668;
MEDLINE=21534947; PubMed=11677668;
MEDLINE=21534947; PubMed=11677668;
MEDLINE=21534947; PubMed=11677668;
MEDLINE=21534947; PubMed=11677668;
Chourant C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
Cronin A., Davies P., Davies R.M., Dowd L., White N., Parrar J.,
Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
Whitehead S., Barrell B.G.;
"Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                       SPECIESS. Typhimurium; STRAIN=LTZ / SGSC1412 / ATCC 700720; MEDLINE=21534948; PubMed=11677609; MCC1elland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
Lucated)
Lucated)
Lucated()
Lucative sugar Kinase, ribokinase family (BC 2.7.1.15) (Putative suryana kinase).
STW3793 OR STY3989.
Salmonella typhimurium, and
Bacteria: Description of the control of the
                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al protein; Complete proteome. 142A0289E2D1B953 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.3%; Score 44; DB 16; Length 306; 47.1%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=06:H1 / CFT073 / ATCC 700928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transferase, Hypothetical
E 306 AA; 33229 MW; 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro, IPR002173; PfkB.
InterPro, IPR002139; Ribokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE008876; AAL22651.1; -. EMBL; AL627280; CAD03201.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               || | ||: ||: ||
84 EKVPCTSSGVAPIFVNA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 EKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00990; RIBOKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 47.13
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 413:848-852(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00294; pfkB; 1
                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=602, 601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Putative ribokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8FKR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
Q8FKR4
```

```
Lalioui L., Le Bouguenec C.C.;
"afa-8 Gene cluster is carried by a pathogenicity island inserted into
the tRNA(Phe) of human and bovine pathogenic Escherichia coli
Walch R.A., Burland V., Plunkett G. III, Redford P., Roesch P., Rasko D., Buckles B.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Rasko D., Buckles B.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

"Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).

EMBL, AR016756; AAN78819.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                  Score 44; DB 16; Length 306; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 314 AA, 34415 MW, 2D5F7342C817E3BB CRC64;
                                                                                                                                                                                                                                                                                                                  33222 MW; 8A0FBEF6BFE493DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 34,4 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 47.1%; Pred. No. 20; 8; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       427 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical 46.8 kDa protein.
C7A10.390.
Arabidopsis thaliana (Mouse-ear cress).
```

; 0

g

ઠે

g

ò

```
STRAIN-A3151,
Kataoka K., Fukui A., Kabayashi M., Yamaguchi K., Suzuki S.;
Kataoka K., Fukui A., Kabayashi M., Yamaguchi K., Suzuki S.;
Kataoka K., Fukui A., Kabayashi M., Yamaguchi K., Suzuki S.;
Fukui Aborita Abo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=1318967; PubMed=11425481;
Peters M., Heinaru A., Nurk A.;
"Plasmid-encoded catalase KatA, the main catalase of Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Hyphomicrobiaceae; Hyphomicrobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1
486 AA; 52238 MW; 6984E02ECEF791AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           506 AA; 57324 MW; F1EAA728C5D41CBE CRC64;
                                                                                                                                                                                                                                                                                               01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Nitrie reductase precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.1%; Score 43; DB 2;
66.7%; Pred. No. 45;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fluorescens strain Cb36.";
FEMS Microbiol. Lett. 200:235-240(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002226; Catalase.
Pfam; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
ProDom; PD000510; Catalase; 1.
PROSITE; PS00438; CATALASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hyphomicrobium denitrificans
                                  208 EEKAEMITAMOSPVV 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1997 (TrEMBLrel. 02, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 EEKTDPTAGAHAPVV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1997 (TrEMBLrel. 02,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U72068; AAB17009.1;
HSSP; P42321; 1M85.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 66.7
Matches 10; Conservative
                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beudomonas fluorescens.
=
=
=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=53399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Catalase isozyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid pAM10.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Cb36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P77924;
                                                                                                                                                                                                                                                                   OSKKH4;
                                                                                                                                                                                                                     Q8KKH4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P77924
                                                                                                                                                   RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
                                                                                                                                                                                          Q8KKH4
                                      .
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SET THE SET OF THE SET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                    Yamada K., Liu S.X., Pham P.K., Banh J., Dale J.M., Goldsmith A.D.,
Jiang P.X., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M.,
Yamada K., Liu S.X., Bowser L., Carninci P., Chen H., Cheuk R.,
Hayashizaki Y., Yu G., Yu S., Bowser L., Kamiya A., Karlin-Neumann G.,
Rawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.,
Narusaka M., Nguyen M., Palm C.J., Sakurai T., Sarou M., Seki M.,
Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W.,
Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W.,
L. Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W.,
Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W.,
R. Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W.,
R. Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W.,
R. Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W.,
R. Phan, IPROS516; Remorin_C.
R. Pfam, PF03763; Remorin_C; I.
R. Pfam; PF03763; Remorin_C; I.
W. Hypothetical protein.
W. SEQUENCE 427 AA, 46788 MW, C8B0192D315DAE41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosida II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
Quach H.L., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.
Yu G., Yuan S., Chen H., Cheuk R., Jones T., Kim C.J., Nguyen M.,
Palm C.J., Shinn P., Southwick A., Tripp M.G., Wu T., Davis R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Bevan M., Terryn N., Vos P., Heijnen L., Mewes H.W., Schueller C.,
Chalwatzis N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.3%; Score 44; DB 10; Length 427; 60.0%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10; Length 427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ecker J.R., Theologis A.;
"Arabidopsis Open Reading Frame (ORF) Clones.";
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46800 MW; 75ACC8E02D90AE54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     427 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.3%; Score 44;
60.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR005516; Remorin C. Pfam; PF03763; Remorin C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z99707; CAB16794.1; -. EMBL; AL161590; CAB80363.1; -. EMBL; AY150393; AAN12938.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 EEKAEMTTAMOSPVV 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel. 05, 01-MAY-1999 (TrEMBLrel. 10, 01-MAR-2003 (TrEMBLrel. 23, Hypothetical protein. C7A10.390 OR AT4G36970.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 60.0.
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                 SEQUENCE FROM N.A.
           NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         023188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
```

ò

ö

Gaps

; 0

Length 486;

Ŋ

ó

ò g

```
09FT45,

01-MAR-2001 (TEMBLE). 16, Created)

01-MAR-2003 (TEMBLE). 16, Last sequence update)

01-MAR-2003 (TEMBLE). 23, Last annotation update)

Hypothetical protein (GPI-anchored protein).

125B15_140.

Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Alcara J.S., Clabault G., Cottet A., Mache R., Mewes H.W., Rudd S.,
Lemcke K., Mayor K.F.X., Quetier F., Salanoubat M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.9%; Score 42; DB 2; Length 211; 61.5%; Pred. No. 29;
                                                                                         51.9%; Score 42; DB 2; Length 210; 57.1%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAINS-SES1401 type PT1658;
Beall B., Gherardi G.;
"The relation of Streptococcus pyogenes sof and emm gene types to genetically distinct strain sets.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AP1543130; ADD36988.1;
                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                        Serum opacity factor precursor (Fragment).
Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 1 1 POTENTIAL.

8 >210 SERUM OPACITY FACTOR.

210 210 AM, 199C89EECF260B6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211 AA; 21367 MW; F5475DDC6A084FE6 CRC64;
                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL. SERUM OPACITY FACTOR.
                                                                                                                                                                                                                                                                211 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         436 AA
                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
SEQUENCE FROM N.A.
EU Arabidopsis sequencing project;
                                                                                                                                                                                     103 EEKTPKTVTSSTPV 116
                                                                                                                                                       2 EEKTPLTTAAXAPV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 EEKTPKTATSSAP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 EEKTPLTTAAXAP 14
                                                                                                                         8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Conservative
                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
>211
211
                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>ئ</u> و
                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus.
                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
NON TER
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TER
                                              NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON TER
SIGNAL
                                                                                                                                                                                                                                                              9X6X8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9FT45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal
                                                                                                                                                                                                                                RESULT 14
Q9X6X8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
Q9FT45
                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
   SFFF
                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=4470-96; TISSUE=Blood;
STRAIN=4470-96; TISSUE=Blood;
Beall B., Gherardi G., Lovgren M., Tyrrell G., Facklam R., Forwick B.;
Predictions of M serotype, anti-opacity factor type, and highly related strain sets based upon the variable emm and sof gene sequences.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF179217; AAD55775.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gruithuijsen Y.K., Beuken E., Bruggeman C.A., Vink C.;
"Rat cytomegalovirus R89 is a highly conserved gene which expresses a spliced transcript.";
Virus Res. 69:119-130(2000).
EMBL, AF232689; ARF99111.1;
-. SEQUENCE 1240 AA; 125612 MW; 33B6C13DC6A272B0 CRC64;
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Maastricht,
MEDLINE-20366325; PubMed=10906222;
Vink C., Beuken E., Bruggeman C.A.;
"Complete DNA sequence of the rat cytomegalovirus genome.";
J. Virol. 74:7656-7665(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.1%; Score 43; DB 12; Length 1240; 64.3%; Pred. No. 1.2e+02;
              DB 2; Length 506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pyogenes.
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Muromegalovirus.
NCBI_TaxID=79700;
                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210 AA.
                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Serum opacity factor precursor (Fragment).
                                                                                                                                                                                                                                                                           Rat cytomegalovirus (strain Maastricht).
               Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-OCT-2002 (TrEMBLrel. 22, Last ann
                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Maastricht;
MEDLINE=20473137; PubMed=11018281;
                                            0;
              Query Match 53.1%;
Best Local Similarity 71.4%;
Matches 10; Conservative
                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         570 EERRELTTAGSAPV 583
                                                                         5 TPLTTAAXAPVVXN 18
                                                                                                       11 THLTTEAGAPVVDN 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 EEKTPLTTAAXAPV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 64.3
Matches 9; Conservative
                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus.
NCBI_TaxID=1314;
                                                                                                                                                                                  . 8НМД60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                    09DWH8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09RNU2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9RNU2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
Q9RNU2
                                                                                                                                                    RESULT 12
```

ઠે

```
genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09SE04
                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                        09SE04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
   ઠે
                                                                                                                                                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                Gaps
                                                STRAIN=cv. Columbia;
Seki M., Idad K., Satou M., Sakurai T., Akiyama K., Ishida J.,
Seki M., Idad K., Satou M., Sakurai T., Akiyama K., Ishida J.,
Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
Hayashizaki Y., Shinozaki K.;
"Arabidopsis thaliana full-length cDNA.";
Submitted (NOV-2012) to the EMBL/GenBank/DDBJ databases.
EMBL; AL132972; CAC07928.1;
EMBL; AL17689; BAC42264.1;
InterPro; IPR000903; Nmt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                  DB 10; Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=A3(2);
Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murphy L., Harris D.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
    Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                     Hypothetical protein. –
SEQUENCE 436 AA; 48073 MW; 83FD94879F9855DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          487 AA
                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                  90;
                                                                                                                                                                                                                                                                                                   Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                              395 EEKTPVEKKTGVPVVKKA 412
                                                                                                                                                                                                                                                                                                                                                               2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                   51.9%;
                                                                                                                                                                                                         Pfam; PF02469; Fasciclin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KATA OR SC00379 OR SCF62.05.
                                                                                                                                                                                                                      SMART; SM00554; FAS1; 2.
PROSITE; PS00976; NMT_2; 1.
                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 50.04
Local 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Catalase (EC 1.11.1.6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=A3(2) / M145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=A3 (2)
                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O9RJK9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O9RJK9;
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9RJK9
      g
                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                        -i- FUNCTION: OCCURS IN ALMOST ALL AEROBICALLY RESPIRING ORGANISMS AND SERVES TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (Rice).
Oryza sativa (Rice).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=98369102; PubMed=9701579;
Himelblau E., Mira H., Lin S.J., Culotta V.C., Penarrubia L., Amasino R.M.;
"Identification of a functional homolog of the yeast copper homeostasis gene ATX1 from Arabidopsis.";
Plant Physiol. 117:1227-1234(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 10; Length 132;
Pred. No. 26;
1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     16; Length 487;
                                                                                                                                                                                                                                                                                                                  Heme; Hydrogen peroxide; Iron; Oxidoreductase; Peroxidase; Complete proteome. SEQUENCE 487 AA; 55116 MW: 9131314890ENBCART AMA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mira H., Penarrubia L.;
"Copper chaperone from Oryza sativa.";
"Copper (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF1986526; AAF15285.1; -.
HSSP; O00244; 1FE0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interrio; .....
PF6am; PF00403; HMA; 1.
PROSTIE; PS50846; HMA 2; 1.
PROSTIE; P3 AA; 13094 MW; 7176EF95350A8231 CRC64;
                                                                                       PEROXIDE (BY SIMILARITY).
--- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
BEL, AL939105; CABS320.1; -.
HSSP; P42321; 1M85.
InterPro; IPR002226; Catalase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation updat. Copper chaperone homolog CCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42; DB 1
Pred. No. 67;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                             PEAM; PF00199; catalase; 1.
PRINTS; PR00067; CATALASE.
PRODUIT: PD00510; Catalase; 1.
PROSITE; PS00437; CATALASE 1; 1.
PROSITE; PS00438; CATALASE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gramene; Q9SE04; -.
InterPro; IPR006121; HeavyMe_tr:
InterPro; IPR006191; Metal_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 EAAPPTTTÄÄEÄPAIAAÄ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                     51.9%;
69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 50.v.
Pest Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 PLTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 PLTTVAGAPVPDN 20
coelicolor A3(2).";
Nature 417:141-147(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
```

ó

```
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RE03056p.
CG30480 OR CG18373.
Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=IM2 / ATCC 51768 / DSM 7523;
PubMed=11792869;
                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                617 ESATPATTATATPKEDNA 634
                                                                                                                                                                                                                                                                  Conserved within P. aerophilum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                      Thermoproteaceae; Pyrobaculum NCBI_TaxID=13773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.6%;
                                                                                                                                                                                                                       (TrEMBLrel. 20, (TrEMBLrel. 20, 1 (TrEMBLrel. 23, 1
                                       Similarity 72.7%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 22, (TrEMBLrel. 22, (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 50.0
Matches 9; Conservative
                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                              454 TPLTTSGNAPV 464
                                                                                              5 TPLTTAAXAPV 15
                                                                                                                                                                                                                                                                                              Pyrobaculum aerophilum.
             516 AA;
                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Complete proteome. SEQUENCE 516 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  aerophilum.";
                                                                                                                                                                                                                                                                                                                                                                                                                        Miller J.H.;
                                                                                                                                                                                                                        01-MAR-2002
                                                                                                                                                                                                                                     01-MAR-2002
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                          Query Match
                                                                                                                                                                                                                                                                               PAE0040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8MT63;
                                                                                                                                                                                            O8ZZX0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8MT63
                                                                                                                                                              RESULT 20
Q8ZZX0
ID Q8ZZX
                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28MT63
                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=ATCC 33913 / NCPPB 528;

MEDINE=2202145; PubMed=12024217;

MADINE=20202145; PubMed=12024217;

A a Silva A.C.R., Ferro J.A., Rethach F.C., Farah C.S., Furlan L.R.,

A da Silva A.C.R., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,

A lves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,

Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

Carcelli R.M.B., Coulinho L.L., Cursino-Santos J.R., El-Dorry H.,

Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

Formighieri E.F., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F.!, Tarkita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

Setubal J.C., Kitajima J.P.,

Trinded dos Santos M., Truffi D., Tsai S.M., White F.F.,

Setubal J.C., Kitajima J.P.,

"Comparison of the genomes of two Xanthomonas pathogens with differing

Thost specificities."

Nature 417,459-463(2002).

EMBL, AED12360, AAM41763.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                        Hidaka T., Hidaka M., Kuzuyama T., Seto H., "Sequence of a P-methyltransferase encoding gene isolated from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                  bialaphos-producing streptomyces hygroscopicus.",
Gene 158:149-150(1995).
-!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
EMBL, DJ7871; BRAG07116.1; -.
HSSP; P56533; 1A4S.
                                                                                                        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 417;
85;
                                                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Oxidoreductase.
SEQUENCE 417 AA; 43406 MW; 9E8714F4FB654B47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  516 AA.
             417 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                        InterPro; IPR002086; Aldehyde_dehydr.
Pfam; PF00171; aldedh; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
                                                                                                                                                                                                                                                                                                                                                                                            50.6%; Score 41; 52.9%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xanthomonas campestris (pv. campestris)
                                        Created)
              PRT;
                                                                                                                                                                                           MEDLINE=95309717; PubMed=7789803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 EKTPLTALAFAELLIEA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 EKTPLTTAAXAPVVXNA 19
                                                    01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2003 (TrEMBLrel. 23, Hypothetical protein.
                                                                                              Streptomyces hygroscopicus.
                                                                                                                                                                                                                                                                                                                                                                                                                      9; Conservative
             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                     01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PilYl protein.
PILY1 OR XCC2489.
                                                                                                                                       NCBI_TaxID=1912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=340;
                                                                                                                                                                               STRAIN-SF1293
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8P7W8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 19
Q8P7W8
054272
                 ò
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                       Score 41; DB 16; Length 516;
Pred. No. 1.1e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41; DB 17; Length 663;
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71372 MW; 216F07B821B78B76 CRC64;
53416 MW; 88A17A8B40B96578 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl Acad. Sci. U.S.A. 99:984-989 (2002).
BMBL, AE009747, AAL62519.1, -.
InterPro; IRR001064; Crystallin.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
```

```
Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9U3E3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9U3E3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F56F12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 none;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9U3E3
     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RG STRAIN-Berkeley;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans G.A., Chen L.X.,

George R.A., Lewis S.E., Richards S. Ashburner M. Henderson S.N.,

Button G.G., Wortenan J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Bardon R.C., Regers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Fennicch C., Baldwin D.,

RA Ballew R.M., Bauu A., Baxendale J.P., Bhandari D., Belshakov S.,

Ra Ballew R.M., Bauu A., Baxendale J.P., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Bauu B.P., Barnel B.P., Bhandari D., Bolshakov S.,

RA Burtis R.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Carly J.M., Cavley S., Dahlke C., Davengort L.B., Davies P., E.,

Burtis R.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cavley S., Dahlke C., Davengort L.B., Davies P., List A.

A cherry J.M., Cabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Googe C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Weil M.-H., Ibegwan C.,

A Jalli M., Kalubh F., Karpen G.H., Ke Z., Kennigon J.A., Ketchum K.A.,

A Liu X., Matuei B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Matteri B., Wolntcob H., Wollerd B., Mosheri A.,

Rander S.M., Moy M., Murphy B., Wixph I., Mursh V. Beace M.G.,

Rander S.M., Moy M., Murphy B., Worther E., Wang A.H.,

Rander S., Sirden-Kianos I. C., McLeod M.P., Misser M. Suiber E., Shand R.,

Rander S., Sirden-Kianos I. Simpson M., Strong S., You C., Steheletor M., Strong S., You C., Steheletor M., Shang S., You C., Steheletor M., Weinsteck M., Weinsteck M., Weinsteck M., Weinsteck M.,

Rander S.M., Woodage T., Worlek M., Wollek 
                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                     Length 920;
                                                                                                Query Match 50.6%; Score 41; DB 5; Length 920
Best Local Similarity 53.3%; Pred. No. 1.9e+02;
Matches 8; Conservative 2; Mismatches 5; Indels
               FlyBase; FBGN0050480; CG30480.
InterPro; IPR002052; N6 Mtase.
PROSITE; PS00092; N6 MTĀSE; 1.
SEQUENCE 920 AA; 101042 MW; 34FFICCBD293AF79 CRC64;
                                                                                                                                                                                                                                                                                                                                                         Last annotation update)
                                                                                                                                                                                                                                                                                                                                          Last sequence update)
                                                                                                                                                                                                                                                                                       920 AA.
                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                    695 EEVTPYNTAPHSPIV 709
                                                                                                                                                                                                                                                                                                                       01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                       2 EEKTPLTTAAXAPVV 16
   EMBL; AY118357; AAM48386.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 287:2185-2195(2000)
                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                          CG30480 OR CG18373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                         CG30480-PA.
                                                                                                                                                                                                                                                                                                          Q8ML93;
                                                                                                                                                                                                                                                                                       OBML93
                                                                                                                                                                                                                                                       RESULT 22
                                                                                                                                                                                                                                                                          OBML93
      80 88 88 80
                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                          ð
```

```
Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y., Baracon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A., Banzon J., M. Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M., Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D., Perriera S., Frise E. Galle R.F., Garg N.S., George R.A., Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J., Pacaleb J., Paragas V., Park S., Patel S., Pfeiffer B., Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F., Stapleron M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; Sequencing of Drosophila melanogaster genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                       Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K. Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith B., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.6%; Score 41; DB 5; Length 920; 53.3%; Pred. No. 1.9e+02; ive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4892AC24257C5203 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=99069613; Pubmed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00092; N6 MTASE; 1.
SEQUENCE 920 AA; 101070 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE003813; AAM68547.1; -. FlyBase; FBgn0050480; CG30480. InterPro; IPR002052; N6 Mtase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           695 EEVTPYNTAPHSPIV 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 53.3%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   investigating biology.";
Science 282:2012-2018(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F56F12.1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ainscough
```

σ

```
Query Match 49.4
Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=340;
                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                      Q8PD69;
                                                                                                                                                                                                                                                                                                                             Q8PD69
                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                  08PD69
  ò
                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-306 / ATCC 13902 / XV 101;
MEDLINE=22022145; PubMed=12024217;
da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
Quaggio R.B., Monterior-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,
Camarotte G., Cannavan F., Cardozo J., Chambergo F., Clapina L.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xanthomonas axonopodis (pv. citri).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Tephritoidea; Tephritidae; Ceratitis.
                                                             DB 5; Length 171;
51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 5; Length 212;
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

Davis T., Yamamoto D.;

Sequence of the fruitless gene in Ceratitis capitata.";

Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF124047; AAF22527.1; --
                                                                                 Indels
         WormPep; F56F12.1; CE23785.
INLEWING: 1PRO03127; Sorb.
SWART; SMO0459; Sorb; 1.
SEQUENCE IT1 AA; 18844 MW; D782482A786F7941 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                22715 MW; DIB7C38FBC5AB8AB CRC64;
                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-077-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein XAC0482.
                                                                                                                                                                                                                                                  Ceratitis capitata (Mediterranean fruit fly)
                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.4%; Score 40; DB 52.9%; Pred. No. 63;
                                                          49.4%; Score 40;
53.3%; Pred. No.
                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 ERSPLTAAAMAAAVAAA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 EKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                               Fruitless protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000210; BTB POZ. Pfam; PF00651; BTB; 1. SMART; SM00225; BTB; 1. PROSITE; PS50097; BTB; 1.
                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2002 (TrEMBLrel. 22,
                                                                                                     5 TPLTTAAXAPVVXNA 19
                                                                                                                        73 TPTTTTAAAPIAAVA 87
                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13,
EMBL; Z82273; CAB54978.1;
                                                                     Local Similarity 53.3
                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 52.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                      212 2
212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=92829;
                                                                                                                                                                                                                                                                                             NCBI_TaxID=7213;
                                                                                                                                                                                                                                                                                                                                                                                                            NON TER
NON TER
SEQUENCE
                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8PQ46
Q8PQ46;
                                                                                                                                                                            Q9U4Y3
                                                                       Best Loca
Matches
                                                                                                                                                       RESULT 24
Q9U4Y3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                     d
                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
```

```
A Silva A.C.R., Ferro J.A., Rethach F.C., Farah C.S., Furlan L.R., A Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F., Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A., Camarotte G. Cannavan F., Carolini M.C., Camargo L.B.A., Ratsuyama P., Coutinho L.L., Cursino-Santos J.R., El-Dorry H., Formighieri E.F., Ferreira R.C.C., Ferro M.I.T., Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F., Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M., Martins E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M., Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R., Spinola L.A.F., Fastia M.A., Tamura R.E., Teixeira E.C., Machado M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D., Silva C., de Souza R.F., Spinola L.A.F., Taxita M.A., Tamura R.E., Teixeira E.C., Machado dos Santos M., Truffi D., Tsai S.M., White F.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H., Paria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T., Formighieri E.F., Franco M.C., Greggio C.C., Gruber A. L. Katsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F., Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M., Martins E.C., Maidanis J., Menck C.F.M., Myaki C.Y., Moon D.H., Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R., Pereira H.A., Rossi A., Sana J.A.D., Silva C., de Souza R.F., Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D., Trindade dos Santos M., Truffi D., Tsai S.M., White F.F., Setubal J.C., Kitajima J.P., Comparison of the genomes of two Xanthomonas pathogens with differing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Comparison of the genomes of two Xanthomonas pathogens with differing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Protecbacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 16; Length 238; 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40, DB 16, Length 238;
Pred. No. 71;
0, Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AE011675, AAM35373.1, -.
InterPro, IPR005834; Hydrolase.
Pfam, PP00702; Hydrolase; 1.
Hypothetical protein, Complete proteome.
SEQUENCE 238 AA, 26418 MW; FA334141562013E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    n; Complete proteome.
26450 MW; B9D14734696D0568 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2002 (TrEMBLrel. 22, Created)
1-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein XCC0471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB 1; Pred. No. 71; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xanthomonas campestris (pv. campestris).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=ATCC 33913 / NCPPB 528;
MEDLINE=22022145; PubMed=12024217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE012145; AAM33789.1; -.
InterPro; IPR005834; Hydrolase.
Pfam; PF00702; Hydrolase; 1.
Hydothetical protein; Complete F
SEQUENCE 238 AA; 26450 MW; B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194 PLLKAARAPVVVN 206
                                                                                                                                                                                                                                                                                                                                                                                                                                        host specificities.";
Nature 417:459-463(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 PLTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3est_Local Similarity 69.2
4atches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             host specificities.";
Nature 417:459-463(2002)
```

```
Science 294:849-852(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=155892;
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=47316;
                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                          Eve-PA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9A4B0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9A4B0
                                                                                                                                                                                                                                                          Q811A1
                                                                                                                                Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 30
                                                                                                                                                                                                                                 RESULT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9A4B0
                                                                                                                                                                                                                                              Q811A1
                                                                                                                                                                                                                                                             줨
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                          임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=EGD-6 / Serovar 1/2a;

MEDLINE=2153729; PubMed=11679669;

A Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

Baquero F., Berche P., Blocker H., Brandt P., Chakraborty T.,

A Charbit A., Checouani F., Couve E., de Daruvar A., Dehoux P.,

Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

Butier L., Goebel W., Gamez-Lopez N., Hain T., Hauf J., Jackson D.,

A Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

A Madueno E., Maltournam A., Mata Vicente J., No E., Nedjari H.,

Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Remmel B., Rose M., Schlueter T., Simos N., Tierrez A.,

Nazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;

"Comparative genomics of Listeria species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                  MEDLINE=99310339; PubMed=10382966; Kawarabayasi Y., Haikawa Y., Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nomura N., Sako Y., Kikuchi H.; "Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 17; Length 252; 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Listeria monocytogenes.
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                         Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
                                                                                                                                                                                                                                                                                                                                                                                     cremarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6.83-101(1999).
EMBL, AP000064; BAA81416.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 252 AA; 25912 MW; 527C1D8A70FFDC14 CRC64;
                                                                                                                         01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
1-NOV-1999 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein APE2401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40;
Pred. No.
                                                                                                       PRT;
                                                                                                                                                                                                                        Desulfurococcaceae; Aeropyrum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein 1mo2028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49.4%;
                                 PLTTAAXAPVVXN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 88.3-
---a 8; Conservative
                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 PLTTAAXAP 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 PLTTAASAP 72
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                               NCBI_TaxID=56636;
                                                                                                                                                                                                Aeropyrum pernix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1639;
                                                                                                                    Q9Y984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 28
                                                                                RESULT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8Y5M9
                                                                                              09Y984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                  ò
                                       셤
                                                                                                        ઠે
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=ATCC 19089 / CB15;
MEDLINE-21173698; PubWed=11259647;
Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Tucson 15010-1001.10;
MEDLINE=22426072; PubMed=12537575;
MEDLINE=22426072; PubMed=12537575;
MEDLINE=22426072; PubMed=12537575;
Gnirke A., Mungall C., Wang A.M., Kronmiller B., Pacleb J., Park Stapleton M., Wan K., George R.A., de Jong P.J., Botas J., Rubin G Celniker S.B.,
"Assessing the impact of comparative genomic sequence data on the functional annotation of the Drosophila genome.";
Genome Biol. 3:RESEARCH0086.1-RESEARCH0086.20(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
                                                                                                                                                                                                                                                                                             .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                              49.4%; Score 40; DB 16; Length 258; 57.1%; Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49.4%; Score 40; DB 5; Length 367; 53.3%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                             Indels
EMBL; ALS91982; CAD00106.1; -.
ListLilat; LM002028; -.
InterPro; IRR002042; S4.
Pfam; PF01479; S4; 1.
SMART; SM00363; S4; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 258 AA: 29682 MW; AE62C55270CFD90F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AY190953; AAO01071.1; -.
SEQUENCE 367 AA; 39464 MW; FDC6800F7040121F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           394 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             367 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 53.3%; Pred. No. 1.1e
8; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :|| :| || ||
303 SPLRSAPTAPAVANA 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein CC2927
CC2927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 TPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                             158 EETELTNAVYAPVI 171
                                                                                                                                                                                                                                                                                                                                                      3 EKTPLITAAXAPVV 16
                                                                                                                                                                                                                                                               Local Similarity 57.1
nes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila littoralis.
```

```
InterPro; IPR007114; MFS.
                                                                                                                                                                                                                                                                         079665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9BLH5;
Q9BLH5;
                                                                                                                                                                                                                                                            079665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                RESULT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 33
                                                                                                                                                                                                                                             079665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9BLH5
     DR DR DR SO S
                                                                                                                                                                                     q
                                                                                                                                                              ò
                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                              ö
Bisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Bly B.,
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
Proc. Natl. Acad. Sci. US.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Taylor K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
Thomson N.R., James K.B., Hacris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
                                                                                                                                                                                                                   Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=A3(2);
Seeger K.J., Harris D.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                      Pfam; PF03929; DUF337; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 394 AA; 42675 MW; 8B11178E174DD18D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2003 (TrEMBLrel. 23, Last annotation update)
Putative transmembrane efflux protein.
                                                                                                                                                                                                    49.4%; Score 40; DB 16; L6
50.0%; Pred. No. 1.2e+02;
Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                         |||||||
315 KTPLTTHLTTPALIDA 330
                                                                                                                                                                                                                                                                      4 KTPLTTAAXAPVVXNA 19
                                                                                                                                            nterPro; IPR005625; DUF337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 417:141-147(2002).
EMBL; AL939114; CAB65584.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=A3(2);
Thomson N.R., Parkhill J.,
                                                                                                                                                                                                              Query Match
Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SC02854 OR SCE20.28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coelicolor A3(2)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                              CC2927; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                       Q9RD97;
                                                                                                                                                                                                                                                                                                                                                                        09RD97
                                                                                                                              FIGR;
                                                                                                                                                                                                                                                                                                                                            RESULT 31
                                                                                                                                                                                                                                                                                                                                                           09RD97
                                                                                                                                                                                                                                                                                                셤
    ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gurtler L.G., Hauser P.H., Eberle J., von Brunn A., Knapp S.,
Zekeng L., Tsague J.M., Kaptue L.,
"A new subtype of human immunodeficiency virus type 1 (MVP-5180) from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                Score 40; DB 16; Length 477; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 498;
                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                        Transmembrane; Complete_proteome. SEQUENCE 477 AA; 47686 MW; 20797B126B148090 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AIDS; Core protein; Polyprotein.
SEQUENCE 498 AA; 55498 MW; 6DE3A29B4E6A17D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Halocynthia roretzi (Sea squirt).
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Halocynthia.
                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 01, Last sequence update) (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 17, Last sequence update) (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; Retroid viruses; Retroviridae; Lentivirus NCBL_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49.4%; Score 40; DB 15; L. 44.4%; Pred. No. 1.5e+02; 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               594 AA
                                                                                                                                                       0; Mismatches
InterPro; IPR005829; Sug_transporter. PROSITE; PS50850; MFS; 1. PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000721; Gag p24.
InterPro; IPR000721; Retrovir p17.
InterPro; IPR001878; Znf CCHC.
Pfam; PP00540; Gag p17; I.
Pfam; PF00607; Gag p24; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=94149848, Pubmed=8107219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EETSPROTSONYPIVTNA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00939; C2HCZNFINGER PRINTS; PR00234; HIVIMATRIX.
                                                                                                                  49.4%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Virol. 68:1581-1585(1994).
EMBL; L20571; AAA44859.1; -.
HSSP; P05888; IAAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00343; ZnF C2HC; 2. PROSITE; PS50158; ZF CCHC; 2
                                                                                                                                                                                                                                                                                                                                                                        01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00098; zf-CCHC; 2
                                                                                                                                                         8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                             5 TPLTTAAXAP 14
                                                                                                                                                                                                                                 19 TPATTAAAP
                                                                                                                                Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                              Gag polyprotein.
GAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HrETR-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=7729
                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cameroon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119
                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
```

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OBMLP2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8MLP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8MLP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RKARNANBEREEEEE,

RARANANBEREEEEEEEE,

RAGAMEN B.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adamstides P.G., Scherer S.E., Li P.W., Hookins R.A., Galle R.E.,

RA George R.A., Lewis S.E., Richards S.D., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeififer B.D.,

RA Abril J.F., Abbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Bessley B.M.,

RA Besson K.Y., Benges P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.B., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan W.B., Bunke C., Borkettier P., Brotcher A., Cadieu B., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.W., Cawley S., Dahlke C., Perraz C., Perriera S., Fleischmann M.,

RA Fosler C., Gabrielian A.E., Garrell J.H., Gu Z., Galbart W.M., Glasser K.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mosherson D.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mosherson D.,

RA Lasko P. Lei Y., Levitsky A.A., Liu J., Li Z., Liang Y., Lin X.,

RA Liako P., Lei Y., Levitsky A.A., Liu J., Li Z., Liang Y., Lin X.,

RA Liako P., Lei Y., Levitsky A.A., Liu J., Li Z., Liang Y., Lin X.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shiee B.C., Siden-Kiamos I., Simpson M., Strong R., Scheeler F., Shen H.,

Rabler R., Spier-Kiamos I., Shampson M., Schoeler F., Shen H.,

Rabler R., Siden-Kiamos I., Shampson M., Schoeler F., Shen H.,

Rabler R., Sheller R., Sheller R., Strong R., Schoeler F., Shen H.,

Rabler R., Siden-Kabayan H.,
                                             "New neural marker genes expressing in subsets of embryonic neural cells of the ascidian, Halocynthia roretzi.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endoptera; Bidopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                         49.4%; Score 40; DB 5; Length 594; 46.7%; Pred. No. 1.8e+02; ive 3; Mismatches 5; Indels
                                                                                                                                                                                                                           63686 MW; 193CDE2B14216920 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                          788 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                        HSSP, P19339; ZSXL,
InterPro, IPR002343; Hud_Sxl_RNA.
InterPro, IPR000504; RNA_rec_mot
                                                                                              EMBL; AB047035; BAB40781.1; -.
                                                                                                                                                    Pfam; PF00076; rrm; 3.
PRINTS; PR00961; HUDSXLRNA.
SMART; SN00360; RRM; 3.
PROSITE; PS50102; RRM; 3.
SEQUENCE 594 AA; 63686 MW.
                                                                                                                                                                                                                                                                                                                                             ||:|| ||: ||:
483 TPITTTQGAPALVNS 497
                                                                                                                                                                                                                                                                                                                           5 TPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 46.74
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
               SEQUENCE FROM N.A.
Yagi K., Makabe K.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MACR-60C protein.
MACR-60C OR CG4356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=BERKELEY
                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9W180
                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 34
Q9W180
                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                             8
```

```
REPLINE=20196006; PubMed=10731132;

KERAIN=Berkeley:

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Ananatides P.G., Scherer S.E., Holt R.A., Evans C.A., Galle R.F.,

RA Ananatides P.G., Scherer S.E., Holt R.A., Evans C.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Stricon G.G., Wortenn J.R., Yandell M.D., Zhang Q., Chen L.K.,

RA Brandon R.C., Rogers Y.-H.C., Blazej K.G., Champe M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Barcer B.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Berkova D., Botchan M.R., Bouck J., Brekstein P., Brottier P.,

RA Glerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Durbin K.J. Evangelista C.C., Mays A.D., Dew I., Dietz S.M.,

RA Durbin K.J., Evangelista C.C., Rerraz C., Ferriera S., Fleischmann W.,

RA Harris N.L., Harvey D., Heinan T.J., Wei M.-H., Ibegwam C.,

RA Harris N.L., Harvey D., Heinan T.J., Wei M.-H., Ibegwam C.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

Alali M., Ralush F., Karpen G.H., Ke Z., Kanlison J.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Monut S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nolson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
SVITEKABS R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yang R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhao B. Zhao B. X.H., Zhong F.N., Zhong W., Zhu X., Zhu S., Zhu X., Zhu S., Zhu X., Smith H.O. Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; Since Sange acquence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                     Science 287:2185-2195(2000).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40; DB 5; Length /00, Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AE003464; AAF47197.1; ...
FlyBase; FBGD000037; mAcR-60C.
InterPro; IPR000276; GPCR_Rhodpsn.
Fam; PF0001; 7tm 1; 1.
PRINTS; PR00237; GPROTEIN RECEP F1 1; 1.
PROSITE; PS50262; GPROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Receptor; Transmembrane.
SEQUENCE 788 AA; 84791 MW; AD8476D9F52AB522 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           805 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   602 EDGPTTTAAAAPLASAA 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 EKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
```

```
NCBI_TaxID=8330;
                                                                                                             FISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-FVB/N;
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8CGF1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8CGF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        002006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 38
002006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 37
      GERTHAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                 Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
A Bvans C.A., Gocayne J.D., Amanatides P.G., Breandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
A Perriers S., Frise E., Galle R.F., Garg N.S., George R.A.,
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
Pacleb J., Paragas V., Park S., Puri V., Richards S., Scheeler F.,
A Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
Sequencing of Drosophila melanogaster genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., She Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier B., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter B., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng I., Zheng K.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zha Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.; Smith H.O., Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Maisra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Tupy J.L., Drydadla R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Mhitfield E., Shaburner M., Gelbart W.M., Rubin G.M., Mnigall C.J., Lewis S.E., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.4%; Score 40; DB 5; Length 805; 52.9%; Pred. No. 2.5e+02; ive 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00237; GPCRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
SEQUENCE 805 AA; 86623 MW; 97A9229CAA5BBED8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     846 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE003464; AAM68310.1; -. FlyBase; FBE0000037; mAcR-60C. ILTerPro; IPR000276; GPCR_Rhodpsn. Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         619 EDGPTTTAAAAPLASAA 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 EKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 06, TrEMBLrel. 06, (TrEMBLrel. 23,
                                                                                                                                                                          Science 287:2185-2195(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1998 (
01-JUN-1998 (
01-MAR-2003 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , 775750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     057577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 36
057577
1D 05757
AC 05757
DT 01-JU
DT 01-JU
      ઠે
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Cynops pyrrhogaster (Japanese common newt).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49.4%; Score 40; DB 11; Length 1266; 50.0%; Pred. No. 3.9e+02; ive 3; Mismatches 6; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49.4%; Score 40; DB 13; Length 846; 52.9%; Pred. No. 2.6e+02; ive 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Strausberg R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC040387; AAH40387.1; -.
SEQUENCE 1266 AA; 142340 MW; 96687B52C3D229D2 CRC64;
                                                                                                                                                                             Mizuno M., Takabatake T., Takahashi T.C., Takeshima K.; "pax-6 gene expression in newt eye development."; Dev. Genes Evol. 207:167-176(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 002006;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Fruit [IJ retrotransposon ninja DNA, complete sequence
(Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59D599C035A1DDB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1360 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1266 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Last sequ
01-MAR-2003 (TrEMBLrel. 23, Last anno
Similar to PTPL1-associated RhoGAP 1.
Mus muscullus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1185 EEKTALPSIAVPPVLVHA 1202
                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00041; fn3; 2.
Pfam; PF00047; ig; 5.
SMART; SM00060; FN3; 2.
PROSITE; PS5085; IG LIKE; 3.
Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92544 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 EEKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              799 ETTPLTEPEKAPVEENS 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 EKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                           InterPro; IPR003961; FN III.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig c2.
InterPro; IPR03006; Ig MHC.
                                                                                                                                                                                                                                                            EMBL; D85084; BAA24033.1; -. HSSP; P56276; 1TLK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 50.0 tes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
```

```
Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      003462
ID 00
AC 00
DT 01
DT 01
MEDIATURE 20196066; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A Sutton G.G., Wortman J.R., Yandall M.D., Zhang Q., Chen L.X.,
Brandon R.C., Bogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,
Ballew R.M., Bouchan M.R., Bourd J., Borskein P., Bottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center P., Dunkov B.C.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Harris N.L., Harvey D., Heiman T.J., Wennison J.R., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Krafe C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
                                                                                                                                                                                                                                                                                                                                   ö
                                                                                      STRAIN=white-chocolate; TISSUE=Body;
MEDLINE=96525483; PubNed=8925473;
OGUTA K., Takechi S., Nakayama T., Yamamoto M.;
"Molecular structure of the transposable element ninja in Drosophila
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).

Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.

NCBI_TaxID=7227;
             Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                        Length 1360;
                   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7240;
                                                                                                                                                                                                                                                                                                       49.4%; Score 40; DB 5; Length 136
47.1%; Pred. No. 4.2e+02;
ive 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                               1360 AA; 150936 MW; DF2021C8DA4AFAE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1399 AA
                                                                                                                                     simulans.",
Genes Genet. Syst. 71:1-8(1996).
EMBL, D93207, BAS57030.1; -.
MENOPS; A17.001; -.
FlyBase; FBGN0044186; Dsim\ninja\pol.
InterPro; IPR001878; Zaf CCHC.
Pfam; PR00093; Z-CCCHC; I.
PRIWTS; PR00339; Z-CCHC; I.
SWART; SM00343; ZnF CZHC; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                            101 EATPITTASQQPASSGA 117
                                                                                                                                                                                                                                                                                                                                                            3 EKTPLTTAAXAPVVXNA 19
                                                                                                                                                                                                                                                                                                                    Best Local Similarity 47.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CG31258 protein.
CG31460 OR CG11745.
                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            озунья; озунря
                                                                                                                                                                                                                                                                    NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                  О9VНР9
                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                      29VHPS
                                                                                                                                                                                                                                                                                                                                                                                  g
 ð
```

```
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Siden-Krämog I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Spier E., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q., A.,
R. J., Yeh R.-P., Zaveri J.S., Zhan M., Zhong G., Zhoo Q., Zheng X.H., Myers E.W., Rubin G.M., Venter J.C.;
R. The genome sequence of Drosophila melanogaster.";
R. Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Celniker S.B., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

Redniker S.B., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

Revans C.A., Gocayre J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

A Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

Rerriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

A Pacleb J., Paragas V., Park S., Patel S., Ffeiffer B.,

Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

A Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,

Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

Sequencing of Drosophila melanogaster genome.",

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A., Matthews B.B., Bayraktaroglu L., Campbell K.

Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,

Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,

Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,

Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,

Searle S.M.J., Smith B., Shu S., Smutniak F., Whitfield E.,

Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,

"Annotation of Drosophila melanogaster genome.",

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49.4%; Score 40; DB 5; Length 1399; 53.3%; Pred. No. 4.3e+02; ive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1399 AA; 156378 MW; B18E1A86714A895E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q03462 PRELIMINARY; PRT; 405 AA.
Q03462;
O1-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE003679; AAF54252.3; -. FlyBase; FBQN0051460; CG31460. InterPro; IPR004827; TF_DZIP. PROSITE; PE000036; BZIP BASIC; SEQUENCE 1399 AA; 156378 WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1241 DEQAPYTEAALGPVV 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 EEKTPLTTAAXAPVV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Conservative
```

```
DT 01-WAR-2002 (TrEMBLrel. 20, Last annotation update)

ON OMDUZ HETERODIMERIZING protein 1 (ORPI).

ON OMPI.

ON OMPI.

ON OMPI.

ON OMPI.

ON OMPI.

ON OMEL TAXAD-457;

ENDIADRA JEACH PARICOIGAGE, Andropogneae; Zea.

ON NOEL TAXAD-457;

ON ONEL TAXAD-457;

RA STRANTH-8002; TISSUB-ENDOSPERM;

RA STRANTH-8002; TISSUB-ENDOSPERM;

RA MEDLINE-93200807; PubMed-943334;

RA MEDLINE-93200807; PubMed-943334;

RA MEDLINE-93200807; PubMed-943334;

RA MEDLINE-93200807; PubMed-943334;

RA MEDLINE-93200807; PubMed-9493334;

RA MEDLINE-93200807; PubMed-943334;

RA MEDLINE-93200807; PubMed-943334;

RA MEDLINE-93200807; PubMed-943334;

RA MEDLINE-93200807; PubMed-943334;

CC -1-EUNCTION: A TRANS-ACTING TRANSCRIPTIONAL ACTIVATOR OF 22 KDA ZEIN

CC -1-EUNCTION: A TRANS-ACTING TRANSCRIPTIONAL ACTIVATOR OF 22 KDA ZEIN

CC -1-EUNCTION: A TRANS-ACTING TRANSCRIPTIONAL ACTIVATOR OF 22 KDA ZEIN

CC -1-EUNCTION: A TRANS-ACTING TRANSCRIPTIONAL ACTIVATOR OF 22 KDA ZEIN

CC -1-EUNCTION: A TRANS-ACTING TRANSCRIPTIONAL ACTIVATOR OF 22 KDA ZEIN

CC -1-SUBMIT: BINDS TO THE 02 SITE CONCENSUS SEQUENCE: GATGATATTGR.

CC -1-SUBMIT: ANA34480.1;

CC -1-SUBMIT: ANA34480.1;

CC -1-SUBMIT: PROMOJS, PZIP: 1.

DR FEAS: PROMOJS, PZIP: 1.

DR SWART; SWOMOJS, PZIP: 1.

NA Transcription regulation; Activator; DNA-binding; Nuclear protein;

RT DNA BIND 214 233 BASIC MM; 3983CAABEBECSODI CRC64;

ONLEY MARCH AS A 42320 MW; PROMO MOLES FOR 1; Indels 7; Gaps 1;

DR CONSTRUCT AND CONSERS FOR MS, PROMO MOLES FOR 1; Indels 7; Gaps 1;

DR FEAS: PROMOJS FOR MS, PROMO MOLES FOR 1; INDELS FOR 1; INDELS FOR 12; PASCENCE 405 MS, PROMOJS FOR 12; INDELS FOR
```

Search completed: January 28, 2004, 13:09:22 Job time : 36 secs

8 6

OLESS MAKE BELLE SILL